

SEQUENCE LISTING



<110> Jones, Brian E.
Kolkman, Marc
Leeflang, Chris
Oh, Hiroshi
Poulose, A.J.
Sadlowski, Eugene S.
Shaw, Andrew
van der Kleij, Wilhelmus A.H.
van Marrenwijk, Leo

<120> Serine Proteases, Nucleic Acids Encoding Serine Enzymes and
Vectors and Host Cells Incorporating Same

<130> GC819-2-US/B

<140> US 10/576,331

<141> 2004-11-19

<150> PCT/US2004/039066

<151> 2004-11-19

<150> US 60/523,609

<151> 2003-11-19

<160> 656

<170> PatentIn version 3.2

<210> 1

<211> 1680

<212> DNA

<213> Cellulomonas strain 69B4

<400> 1

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cgtcctgtac	gtcgccacca	ccgacgagga	cgccgtcgag	gaggtcgagg	gcgaaggcgc	540
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caaccccacc	gggaccttcg	ccgggtccag	cttcccgggc	aacgactacg	cgttcgctccg	960
taccggggcc	ggcgtgaacc	tgctggccca	ggtcaacaac	tactccggtg	gccgcgtcca	1020
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cggggtggcac	tgccggcaca	tactgcgct	caactcctcg	gtcacctacc	ccgagggcac	1140
cgtcgcgggc	ctgatccgca	ccaccgtctg	cgccgagccc	ggcgactccg	gtggctcgct	1200
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tggtaccacg	ttcttccagc	cgggtcaaccc	catcctccag	gcgtacggcc	tgaggatgat	1320
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cgacctctac	gtgcagcgt	ggaacggcag	ctcctgggtg	accgtcgccc	agagcacctc	1560
ccccggctcc	aacgagacca	tcacctaccg	cggcaacgcc	ggctactacc	gctacgtggt	1620
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<210> 2

<211> 1488

<212> DNA

<213> Cellulomonas strain 69B4

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ccacgcctgg	ccgagaagct	cgaccccgac	ctcctcgagg	ccatggagcg	cgacctgggc	180
ctcgacgcgg	aggaagccgc	cgccaccctg	gcgttccagc	acgacgcagc	cgagaccggc	240
gaggccctcg	ccgaagagct	cgacgaggac	ttcgccggca	cctgggtcga	ggacgacgtc	300
ctgtacgtcg	ccaccaccga	cgaggacgcc	gtcgaggagg	tcgagggcga	aggcgccacg	360
gccgtcaccg	tcgagcactc	cctggccgac	ctcgaggcct	ggaagaccgt	cctcgacgcc	420
gccctcgagg	gccacgacga	cgtgcccacc	tggtagctcg	acgtcccgc	caacagcgtc	480
gtcgtcgccg	tcaaggccgg	agcccaggac	gtcgccggccg	gcctcgtcga	aggtgccgac	540
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cccaccggga	ccttcgccgg	gtccagcttc	ccgggcaacg	actacgcgtt	cgcccgtaac	780
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cgcggcctga	tcggcaccac	cgtctgcgc	gagcccgccg	actccggtgg	ctcgctgctc	1020
gccggcaacc	aggccaggg	cgtcacgtcc	ggcggtccg	gcaactgccc	caccggtggc	1080
accagcttct	tcagccgggt	caaccccatc	ctccaggcgt	acggcctgag	gatgatcacc	1140
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ggctccaacg	agaccatcac	ctaccgcggc	aacgcgggt	actaccgcta	cgtgggtcaac	1440
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<210> 3

<211> 1404

<212> DNA

<213> Cellulomonas spp.

<400> 3

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accctggcgt	tcagcacga	cgcagccgag	accggcgagg	ccctcgccga	agagctcgac	180
gaggacttcg	ccggcacctg	ggtcgaggac	gacgtcctgt	acgtcgccac	caccgacgag	240
gacgcgtcg	aggaggtcga	gggcgaaggc	gccacggccg	tcaccgtcga	gcactccctg	300
gccgaacctg	aggcctggaa	gaccgtcctc	gacgcggccc	tcgagggcca	cgacgacgtg	360
cccacctgggt	acgtcgacgt	cccgaaccaac	agcgtcgctc	tcgccgtcaa	ggccggagcc	420
caggacgtcg	ccgcggccct	cgtcgaagg	gccgacgtcc	cgtccgacgc	cgtgaccttc	480
gtcgagaccg	acgagacccc	gcggaccatg	ttcgacgtga	tcggcgccaa	cgcctacacc	540
atcggggggc	gcagccgctg	ctcgatcggg	ttcgcggtca	acggcggggt	catcaccgcc	600
ggccactgcg	gccgcaccgg	cgccaccacc	gccaaaccca	ccgggacctt	cgccgggtcc	660

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acgtccggcg	gtcccgga	ctgccgcacc	ggtggcacca	cgttcttcca	gccggtcaac	1020
cccatacctc	aggcgtacgg	cctgaggatg	atcaccacgg	actcgggcag	cagccccggc	1080
cctgcaccga	cctcctgcac	cggtacgcc	cgcaccttca	ccgggaccct	cgcggccggc	1140
cgggcgcgcg	cccagcccaa	cgggtcctac	gtgcagggtc	accggtccgg	gacccacagc	1200
gtgtgcctca	acgggcccctc	cgggtcggac	ttcgacctct	acgtgcagcg	ctggaacggc	1260
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cgcggcaacg	ccggctacta	ccgtacgtg	gtcaacgcgc	cgtccggctc	cggtgcctac	1380
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<210> 4
 <211> 567
 <212> DNA
 <213> Cellulomonas spp.

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gccaacccca	ccgggacctt	cgcggggtcc	agcttcccgg	gcaacgacta	cgcgttcgtc	180
cgtaccgggg	ccggcgtgaa	cctgctggcc	cagggtcaaca	actactccgg	tggccgcgtc	240
cagggtcgccg	ggcacaccgc	ggcccccgtc	ggctcggccg	tgtgccggtc	cgggtcgacc	300
accgggtggc	actgcggcac	catcactgcg	ctcaactcct	cggtcaccta	ccccgagggc	360
accgtccgcg	gcctgatccg	caccaccgtc	tgcgcggagc	ccggcgactc	cgggtggctcg	420
ctgctcgccg	gcaaccaggc	ccagggcgtc	acgtccggcg	gctccggcaa	ctgccgcacc	480
ggtggcacca	cgttcttcca	gccggtaaac	cccatacctc	aggcgtacgg	cctgaggatg	540
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<210> 5
 <211> 83
 <212> DNA
 <213> Cellulomonas strain 69B4

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<210> 6
 <211> 495
 <212> PRT
 <213> Cellulomonas strain 69B4

<400> 6															
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Ala	Thr	Leu	Leu	Ala	Gly	Gly	Met	Ala	Ala	Gln	Ala	Asn	Glu	Pro	Ala
			20					25					30		
Pro	Pro	Gly	Ser	Ala	Ser	Ala	Pro	Pro	Arg	Leu	Ala	Glu	Lys	Leu	Asp
		35					40					45			
Pro	Asp	Leu	Leu	Glu	Ala	Met	Glu	Arg	Asp	Leu	Gly	Leu	Asp	Ala	Glu
	50					55					60				
Glu	Ala	Ala	Ala	Thr	Leu	Ala	Phe	Gln	His	Asp	Ala	Ala	Glu	Thr	Gly
65					70				75						80

<400> 7

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Leu	Asp	Ala	Glu	Glu	Ala	Ala	Ala	Thr	Leu	Ala	Phe	Gln	His	Asp	Ala	35	40	45	
Ala	Glu	Thr	Gly	Glu	Ala	Leu	Ala	Glu	Glu	Leu	Asp	Glu	Asp	Phe	Ala	50	55	60	
Gly	Thr	Trp	Val	Glu	Asp	Val	Leu	Tyr	Val	Ala	Thr	Thr	Asp	Glu		65	70	75	80
Asp	Ala	Val	Glu	Glu	Val	Glu	Gly	Glu	Gly	Ala	Thr	Ala	Val	Thr	Val	85	90	95	
Glu	His	Ser	Leu	Ala	Asp	Leu	Glu	Ala	Trp	Lys	Thr	Val	Leu	Asp	Ala	100	105	110	
Ala	Leu	Glu	Gly	His	Asp	Asp	Val	Pro	Thr	Trp	Tyr	Val	Asp	Val	Pro	115	120	125	
Thr	Asn	Ser	Val	Val	Val	Ala	Val	Lys	Ala	Gly	Ala	Gln	Asp	Val	Ala	130	135	140	
Ala	Gly	Leu	Val	Glu	Gly	Ala	Asp	Val	Pro	Ser	Asp	Ala	Val	Thr	Phe	145	150	155	160
Val	Glu	Thr	Asp	Glu	Thr	Pro	Arg	Thr	Met	Phe	Asp	Val	Ile	Gly	Gly	165	170	175	
Asn	Ala	Tyr	Thr	Ile	Gly	Gly	Arg	Ser	Arg	Cys	Ser	Ile	Gly	Phe	Ala	180	185	190	
Val	Asn	Gly	Gly	Phe	Ile	Thr	Ala	Gly	His	Cys	Gly	Arg	Thr	Gly	Ala	195	200	205	
Thr	Thr	Ala	Asn	Pro	Thr	Gly	Thr	Phe	Ala	Gly	Ser	Ser	Phe	Pro	Gly	210	215	220	
Asn	Asp	Tyr	Ala	Phe	Val	Arg	Thr	Gly	Ala	Gly	Val	Asn	Leu	Leu	Ala	225	230	235	240
Gln	Val	Asn	Asn	Tyr	Ser	Gly	Gly	Arg	Val	Gln	Val	Ala	Gly	His	Thr	245	250	255	
Ala	Ala	Pro	Val	Gly	Ser	Ala	Val	Cys	Arg	Ser	Gly	Ser	Thr	Thr	Gly	260	265	270	
Trp	His	Cys	Gly	Thr	Ile	Thr	Ala	Leu	Asn	Ser	Ser	Val	Thr	Tyr	Pro	275	280	285	
Glu	Gly	Thr	Val	Arg	Gly	Leu	Ile	Arg	Thr	Thr	Val	Cys	Ala	Glu	Pro	290	295	300	
Gly	Asp	Ser	Gly	Gly	Ser	Leu	Leu	Ala	Gly	Asn	Gln	Ala	Gln	Gly	Val	305	310	315	320
Thr	Ser	Gly	Gly	Ser	Gly	Asn	Cys	Arg	Thr	Gly	Gly	Thr	Thr	Phe	Phe	325	330	335	
Gln	Pro	Val	Asn	Pro	Ile	Leu	Gln	Ala	Tyr	Gly	Leu	Arg	Met	Ile	Thr	340	345	350	
Thr	Asp	Ser	Gly	Ser	Ser	Pro	Ala	Pro	Ala	Pro	Thr	Ser	Cys	Thr	Gly	355	360	365	
Tyr	Ala	Arg	Thr	Phe	Thr	Gly	Thr	Leu	Ala	Ala	Gly	Arg	Ala	Ala	Ala	370	375	380	
Gln	Pro	Asn	Gly	Ser	Tyr	Val	Gln	Val	Asn	Arg	Ser	Gly	Thr	His	Ser	385	390	395	400
Val	Cys	Leu	Asn	Gly	Pro	Ser	Gly	Ala	Asp	Phe	Asp	Leu	Tyr	Val	Gln	405	410	415	
Arg	Trp	Asn	Gly	Ser	Ser	Trp	Val	Thr	Val	Ala	Gln	Ser	Thr	Ser	Pro	420	425	430	

Gly Ser Asn Glu Thr Ile Thr Tyr Arg Gly Asn Ala Gly Tyr Tyr Arg
 435 440 445
 Tyr Val Val Asn Ala Ala Ser Gly Ser Gly Ala Tyr Thr Met Gly Leu
 450 455 460
 Thr Leu Pro
 465

<210> 8
 <211> 189
 <212> PRT
 <213> Cellulomonas spp.

<400> 8

Phe Asp Val Ile Gly Gly Asn Ala Tyr Thr Ile Gly Gly Arg Ser Arg
 1 5 10 15
 Cys Ser Ile Gly Phe Ala Val Asn Gly Gly Phe Ile Thr Ala Gly His
 20 25 30
 Cys Gly Arg Thr Gly Ala Thr Thr Ala Asn Pro Thr Gly Thr Phe Ala
 35 40 45
 Gly Ser Ser Phe Pro Gly Asn Asp Tyr Ala Phe Val Arg Thr Gly Ala
 50 55 60
 Gly Val Asn Leu Leu Ala Gln Val Asn Asn Tyr Ser Gly Gly Arg Val
 65 70 75 80
 Gln Val Ala Gly His Thr Ala Ala Pro Val Gly Ser Ala Val Cys Arg
 85 90 95
 Ser Gly Ser Thr Thr Gly Trp His Cys Gly Thr Ile Thr Ala Leu Asn
 100 105 110
 Ser Ser Val Thr Tyr Pro Glu Gly Thr Val Arg Gly Leu Ile Arg Thr
 115 120 125
 Thr Val Cys Ala Glu Pro Gly Asp Ser Gly Gly Ser Leu Leu Ala Gly
 130 135 140
 Asn Gln Ala Gln Gly Val Thr Ser Gly Gly Ser Gly Asn Cys Arg Thr
 145 150 155 160
 Gly Gly Thr Thr Phe Phe Gln Pro Val Asn Pro Ile Leu Gln Ala Tyr
 165 170 175
 Gly Leu Arg Met Ile Thr Thr Asp Ser Gly Ser Ser Pro
 180 185

<210> 9
 <211> 28
 <212> PRT
 <213> Cellulomonas strain 69B4

<400> 9

Met Thr Pro Arg Thr Val Thr Arg Ala Leu Ala Val Ala Thr Ala Ala
 1 5 10 15
 Ala Thr Leu Leu Ala Gly Gly Met Ala Ala Gln Ala
 20 25

<210> 10
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>

<223> primer

<220>

<221> misc_feature

<222> (3)..(3)

<223> n is a, c, g, or t

<400> 10

acnacsggst ggcrgtgcgg cac

23

<210> 11

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<220>

<221> misc_feature

<222> (2)..(17)

<223> n is a, c, g, or t

<400> 11

angngccgcc ggagtcncc

19

<210> 12

<211> 58

<212> PRT

<213> Cellulomonas strain 69B4

<400> 12

Asp Gly Trp Asp Cys Gly Thr Ile Thr Ala Leu Asn Ser Ser Val Thr
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Tyr Pro Glu Gly Thr Val Arg Gly Leu Ile Arg Thr Thr Val Cys Ala
20 25 30
Glu Pro Gly Asp Ser Gly Gly Ser Leu Leu Ala Gly Asn Gln Ala Gln
35 40 45
Gly Val Thr Ser Gly Asp Ser Gly Gly Ser
50 55

<210> 13

<211> 177

<212> DNA

<213> Cellulomonas strain 69B4

<400> 13

acgacggctg ggactgcggc accatcactg cgctcaactc ctcggtcacc taccgagagg 60
gcaccgtccg cggcctgatc cgcaccaccg tctgcgccga gcccggcgac tccggtggct 120
cgctgctcgc cggcaaccag gcccaaggcg tcacgtccgg cgactccggc ggctcat 177

<210> 14

<211> 32

<212> DNA

<213> Artificial Sequence

<220>
 <223> primer

 <400> 14
 cggggtaggt gaccgaggag ttgagcgag tg 32

 <210> 15
 <211> 33
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> primer

 <400> 15
 gctcgccggc aaccaggccc agggcgac gtc 33

 <210> 16
 <211> 34
 <212> DNA
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 <220>
 <223> primer

 <400> 16
 aacggcgggt tcatcaccgc cggccactgc ggcc 34

 <210> 17
 <211> 14
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> N-terminus of the mature chain determined by MALDI-TOF analysis

 <400> 17

 Phe Asp Val Ile Gly Gly Asn Ala Tyr Thr Ile Gly Gly Arg
 1 5 10

 <210> 18
 <211> 189
 <212> PRT
 <213> Cellulomonas strain 69B4

 <400> 18

 Phe Asp Val Ile Gly Gly Asn Ala Tyr Thr Ile Gly Gly Arg Ser Arg
 1 5 10 15
 Cys Ser Ile Gly Phe Ala Val Asn Gly Gly Phe Ile Thr Ala Gly His
 20 25 30
 Cys Gly Arg Thr Gly Ala Thr Thr Ala Asn Pro Thr Gly Thr Phe Ala
 35 40 45
 Gly Ser Ser Phe Pro Gly Asn Asp Tyr Ala Phe Val Arg Thr Gly Ala

50		55		60
Gly Val Asn Leu Leu Ala Gln Val Asn Asn Tyr Ser Gly Gly Arg Val				
65		70		80
Gln Val Ala Gly His Thr Ala Ala Pro Val Gly Ser Ala Val Cys Arg				
	85		90	95
Ser Gly Ser Thr Thr Gly Trp His Cys Gly Thr Ile Thr Ala Leu Asn				
	100		105	110
Ser Ser Val Thr Tyr Pro Glu Gly Thr Val Arg Gly Leu Ile Arg Thr				
	115		120	125
Thr Val Cys Ala Glu Pro Gly Asp Ser Gly Gly Ser Leu Leu Ala Gly				
	130		135	140
Asn Gln Ala Gln Gly Val Thr Ser Gly Gly Ser Gly Asn Cys Arg Thr				
145		150		155
Gly Gly Thr Thr Phe Phe Gln Pro Val Asn Pro Ile Leu Gln Ala Tyr				
	165		170	175
Gly Leu Arg Met Ile Thr Thr Asp Ser Gly Ser Ser Pro				
	180		185	

<210> 19

<211> 184

<212> PRT

<213> Streptomyces griseus

<400> 19

Thr Pro Leu Ile Ala Gly Gly Glu Ala Ile Thr Thr Gly Gly Ser Arg		
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Cys Ser Leu Gly Phe Asn Val Ser Val Asn Gly Val Ala His Ala Leu		
	20	25
Thr Ala Gly His Cys Thr Asn Ile Ser Ala Ser Trp Ser Ile Gly Thr		
	35	40
Arg Thr Gly Thr Ser Phe Pro Asn Asn Asp Tyr Gly Ile Ile Arg His		
	50	55
Ser Asn Pro Ala Ala Ala Asp Gly Arg Val Tyr Leu Tyr Asn Gly Ser		
65	70	75
Tyr Gln Asp Ile Thr Thr Ala Gly Asn Ala Phe Val Gly Gln Ala Val		
	85	90
Gln Arg Ser Gly Ser Thr Thr Gly Leu Arg Ser Gly Ser Val Thr Gly		
	100	105
Leu Asn Ala Thr Val Asn Tyr Gly Ser Ser Gly Ile Val Tyr Gly Met		
	115	120
Ile Gln Thr Asn Val Cys Ala Glu Pro Gly Asp Ser Gly Gly Ser Leu		
	130	135
Phe Ala Gly Ser Thr Ala Leu Gly Leu Thr Ser Gly Gly Ser Gly Asn		
145	150	155
Cys Arg Thr Gly Gly Thr Thr Phe Tyr Gln Pro Val Thr Glu Ala Leu		
	165	170
Ser Ala Tyr Gly Ala Thr Val Leu		
	180	

<210> 20

<211> 174

<212> PRT

<213> Streptomyces fradiae

<400> 20

Ile	Ala	Gly	Gly	Glu	Ala	Ile	Tyr	Ala	Ala	Gly	Gly	Gly	Arg	Cys	Ser	1	5	10	15
Leu	Gly	Phe	Asn	Val	Arg	Ser	Ser	Ser	Gly	Ala	Thr	Tyr	Ala	Leu	Thr	20	25	30	
Ala	Gly	His	Cys	Thr	Glu	Ile	Ala	Ser	Thr	Trp	Tyr	Thr	Asn	Ser	Gly	35	40	45	
Gln	Thr	Ser	Leu	Leu	Gly	Thr	Arg	Ala	Gly	Thr	Ser	Phe	Pro	Gly	Asn	50	55	60	
Asp	Tyr	Gly	Leu	Ile	Arg	His	Ser	Asn	Ala	Ser	Ala	Ala	Asp	Gly	Arg	65	70	75	80
Val	Tyr	Leu	Tyr	Asn	Gly	Ser	Tyr	Arg	Asp	Ile	Thr	Gly	Ala	Gly	Asn	85	90	95	
Ala	Tyr	Val	Gly	Gln	Thr	Val	Gln	Arg	Ser	Gly	Ser	Thr	Thr	Gly	Leu	100	105	110	
His	Ser	Gly	Arg	Val	Thr	Gly	Leu	Asn	Ala	Thr	Val	Asn	Tyr	Gly	Gly	115	120	125	
Gly	Asp	Ile	Val	Ser	Gly	Leu	Ile	Gln	Thr	Asn	Val	Cys	Ala	Glu	Pro	130	135	140	
Gly	Asp	Ser	Gly	Gly	Ala	Leu	Phe	Ala	Gly	Ser	Thr	Ala	Leu	Gly	Leu	145	150	155	160
Thr	Ser	Gly	Gly	Ser	Gly	Asn	Cys	Arg	Thr	Gly	Gly	Thr	Thr			165	170		

<210> 21
 <211> 188
 <212> PRT
 <213> Streptomyces lividans

<400> 21

Asn	Lys	Leu	Ile	Gln	Gly	Gly	Asp	Ala	Ile	Tyr	Ala	Ser	Ser	Trp	Arg	1	5	10	15
Cys	Ser	Leu	Gly	Phe	Asn	Val	Arg	Thr	Ser	Ser	Gly	Ala	Glu	Tyr	Phe	20	25	30	
Leu	Thr	Ala	Gly	His	Cys	Thr	Asp	Gly	Ala	Gly	Ala	Trp	Arg	Ala	Ser	35	40	45	
Ser	Gly	Gly	Thr	Val	Ile	Gly	Gln	Thr	Ala	Gly	Ser	Ser	Phe	Pro	Gly	50	55	60	
Asn	Asp	Tyr	Gly	Ile	Val	Gln	Tyr	Thr	Gly	Ser	Val	Ser	Arg	Pro	Gly	65	70	75	80
Thr	Ala	Asn	Gly	Val	Asp	Ile	Thr	Arg	Ala	Ala	Thr	Pro	Ser	Val	Gly	85	90	95	
Thr	Thr	Val	Ile	Arg	Asp	Gly	Ser	Thr	Thr	Gly	Thr	His	Ser	Gly	Arg	100	105	110	
Val	Thr	Ala	Leu	Asn	Ala	Thr	Val	Asn	Tyr	Gly	Gly	Gly	Asp	Val	Val	115	120	125	
Gly	Gly	Leu	Ile	Gln	Thr	Thr	Val	Cys	Ala	Glu	Pro	Gly	Asp	Ser	Gly	130	135	140	
Gly	Ser	Leu	Tyr	Gly	Ser	Asn	Gly	Thr	Ala	Tyr	Gly	Leu	Thr	Ser	Gly	145	150	155	160
Gly	Ser	Gly	Asn	Cys	Ser	Ser	Gly	Gly	Thr	Thr	Phe	Phe	Gln	Pro	Val	165	170	175	
Thr	Glu	Ala	Leu	Ser	Ala	Tyr	Gly	Val	Ser	Val	Tyr					180	185		

<210> 22
 <211> 188

<212> PRT
<213> Streptomyces coelicolor

<400> 22

```
Asn Lys Leu Ile Gln Gly Gly Asp Ala Ile Tyr Ala Ser Ser Trp Arg
1      5      10      15
Cys Ser Leu Gly Phe Asn Val Arg Thr Ser Ser Gly Ala Glu Tyr Phe
      20      25      30
Leu Thr Ala Gly His Cys Thr Asp Gly Ala Gly Ala Trp Arg Ala Ser
      35      40      45
Ser Gly Gly Thr Val Ile Gly Gln Thr Ala Gly Ser Ser Phe Pro Gly
      50      55      60
Asn Asp Tyr Gly Ile Val Gln Tyr Thr Gly Ser Val Ser Arg Pro Gly
65      70      75      80
Thr Ala Asn Gly Val Asp Ile Thr Arg Ala Ala Thr Pro Ser Val Gly
      85      90      95
Thr Thr Val Ile Arg Asp Gly Ser Thr Thr Gly Thr His Ser Gly Arg
      100     105     110
Val Thr Ala Leu Asn Ala Thr Val Asn Tyr Gly Gly Gly Asp Val Val
      115     120     125
Gly Gly Leu Ile Gln Thr Thr Val Cys Ala Glu Pro Gly Asp Ser Gly
      130     135     140
Gly Ser Leu Tyr Gly Ser Asn Gly Thr Ala Tyr Gly Leu Thr Ser Gly
145     150     155     160
Gly Ser Gly Asn Cys Ser Ser Gly Gly Thr Thr Phe Phe Gln Pro Val
      165     170     175
Thr Glu Ala Leu Ser Ala Tyr Gly Val Ser Val Tyr
      180     185
```

<210> 23
<211> 189
<212> PRT

<213> Streptomyces albogriseolus

<400> 23

```
Thr Lys Leu Ile Gln Gly Gly Asp Ala Ile Tyr Ala Ser Ser Trp Arg
1      5      10      15
Cys Ser Leu Gly Phe Asn Val Arg Ser Ser Ser Gly Val Asp Tyr Phe
      20      25      30
Leu Thr Ala Gly His Cys Thr Asp Gly Ala Gly Thr Trp Tyr Ser Asn
      35      40      45
Ser Ala Arg Thr Thr Ala Ile Gly Ser Thr Ala Gly Ser Ser Phe Pro
      50      55      60
Gly Asn Asp Tyr Gly Ile Val Arg Tyr Thr Gly Ser Val Ser Arg Pro
65      70      75      80
Gly Thr Ala Asn Gly Val Asp Ile Thr Arg Ala Ala Thr Pro Ser Val
      85      90      95
Gly Thr Thr Val Ile Arg Asp Gly Ser Thr Thr Gly Thr His Ser Gly
      100     105     110
Arg Val Thr Ala Leu Asn Ala Thr Val Asn Tyr Gly Gly Gly Asp Ile
      115     120     125
Val Ser Gly Leu Ile Gln Thr Thr Val Cys Ala Glu Pro Gly Asp Ser
      130     135     140
Gly Gly Pro Leu Tyr Gly Ser Asn Gly Thr Ala Tyr Gly Leu Thr Ser
```

145		150		155		160									
Gly	Gly	Ser	Gly	Asn	Cys	Ser	Ser	Gly	Gly	Thr	Thr	Phe	Phe	Gln	Pro
		165		170		175									
Val	Thr	Glu	Ala	Leu	Ser	Ala	Tyr	Gly	Val	Ser	Val	Tyr			
		180		185											

<210> 24
 <211> 188
 <212> PRT
 <213> Streptomyces griseus

<400> 24

Thr	Lys	Leu	Ile	Ser	Gly	Gly	Asp	Ala	Ile	Tyr	Ser	Ser	Thr	Gly	Arg
1				5					10					15	
Cys	Ser	Leu	Gly	Phe	Asn	Val	Arg	Ser	Gly	Ser	Thr	Tyr	Tyr	Phe	Leu
		20					25						30		
Thr	Ala	Gly	His	Cys	Thr	Asp	Gly	Ala	Thr	Thr	Trp	Trp	Ala	Asn	Ser
	35					40						45			
Ala	Arg	Thr	Thr	Val	Leu	Gly	Thr	Thr	Ser	Gly	Ser	Ser	Phe	Pro	Asn
	50				55				60						
Asn	Asp	Tyr	Gly	Ile	Val	Arg	Tyr	Thr	Asn	Thr	Thr	Ile	Pro	Lys	Asp
65				70				75					80		
Gly	Thr	Val	Gly	Gly	Gln	Asp	Ile	Thr	Ser	Ala	Ala	Asn	Ala	Thr	Val
		85						90					95		
Gly	Met	Ala	Val	Thr	Arg	Arg	Gly	Ser	Thr	Thr	Gly	Thr	His	Ser	Gly
	100						105						110		
Ser	Val	Thr	Ala	Leu	Asn	Ala	Thr	Val	Asn	Tyr	Gly	Gly	Gly	Asp	Val
	115				120						125				
Val	Tyr	Gly	Met	Ile	Arg	Thr	Asn	Val	Cys	Ala	Glu	Pro	Gly	Asp	Ser
	130			135				140							
Gly	Gly	Pro	Leu	Tyr	Ser	Gly	Thr	Arg	Ala	Ile	Gly	Leu	Thr	Ser	Gly
145				150				155						160	
Gly	Ser	Gly	Asn	Cys	Ser	Ser	Gly	Gly	Thr	Thr	Phe	Phe	Gln	Pro	Val
		165					170						175		
Thr	Glu	Ala	Leu	Ser	Ala	Tyr	Gly	Val	Ser	Val	Tyr				
		180					185								

<210> 25
 <211> 188
 <212> PRT
 <213> Streptomyces griseus

<400> 25

Val	Leu	Gly	Gly	Gly	Ala	Ile	Tyr	Gly	Gly	Gly	Ser	Arg	Cys	Ser	Ala
1				5				10						15	
Ala	Phe	Asn	Val	Thr	Lys	Gly	Gly	Ala	Arg	Tyr	Phe	Val	Thr	Ala	Gly
	20						25					30			
His	Cys	Thr	Asn	Ile	Ser	Ala	Asn	Trp	Ser	Ala	Ser	Ser	Gly	Gly	Ser
	35					40					45				
Val	Val	Gly	Val	Arg	Glu	Gly	Thr	Ser	Phe	Pro	Thr	Asn	Asp	Tyr	Gly
	50				55			60							
Ile	Val	Arg	Tyr	Thr	Asp	Gly	Ser	Ser	Pro	Ala	Gly	Thr	Val	Asp	Leu
65				70				75					80		
Tyr	Asn	Gly	Ser	Thr	Gln	Asp	Ile	Ser	Ser	Ala	Ala	Asn	Ala	Val	Val
		85					90						95		

Gly Gln Ala Ile Lys Lys Ser Gly Ser Thr Thr Lys Val Thr Ser Gly
 100 105 110
 Thr Val Thr Ala Val Asn Val Thr Val Asn Tyr Gly Asp Gly Pro Val
 115 120 125
 Tyr Asn Met Gly Arg Thr Thr Ala Cys Ser Ala Gly Gly Asp Ser Gly
 130 135 140
 Gly Ala His Phe Ala Gly Ser Val Ala Leu Gly Ile His Ser Gly Ser
 145 150 155 160
 Ser Gly Cys Ser Gly Thr Ala Gly Ser Ala Ile His Gln Pro Val Thr
 165 170 175
 Lys Ala Leu Ser Ala Tyr Gly Val Thr Val Tyr Leu
 180 185

<210> 26
 <211> 190
 <212> PRT
 <213> Streptomyces fradiae

<400> 26

Gln Arg Glu Val Ala Gly Gly Asp Ala Ile Tyr Gly Gly Gly Ser Arg
 1 5 10 15
 Cys Ser Ala Ala Phe Asn Val Thr Lys Asn Gly Val Arg Tyr Phe Leu
 20 25 30
 Thr Ala Gly His Cys Thr Asn Leu Ser Ser Thr Trp Ser Ser Thr Ser
 35 40 45
 Gly Gly Thr Ser Ile Gly Val Arg Glu Gly Thr Ser Phe Pro Thr Asn
 50 55 60
 Asp Tyr Gly Ile Val Arg Tyr Thr Thr Thr Thr Asn Val Asp Gly Arg
 65 70 75 80
 Val Asn Leu Tyr Asn Gly Gly Tyr Gln Asp Ile Ala Ser Ala Ala Asp
 85 90 95
 Ala Val Val Gly Gln Ala Ile Lys Lys Ser Gly Ser Thr Thr Lys Val
 100 105 110
 Thr Ser Gly Thr Val Ser Ala Val Asn Val Thr Val Asn Tyr Ser Asp
 115 120 125
 Gly Pro Val Tyr Gly Met Val Arg Thr Thr Ala Cys Ser Ala Gly Gly
 130 135 140
 Asp Ser Gly Gly Ala His Phe Ala Gly Ser Val Ala Leu Gly Ile His
 145 150 155 160
 Ser Gly Ser Ser Gly Cys Thr Gly Thr Asn Gly Ser Ala Ile His Gln
 165 170 175
 Pro Val Arg Glu Ala Leu Ser Ala Tyr Gly Val Asn Val Tyr
 180 185 190

<210> 27
 <211> 190
 <212> PRT
 <213> Streptomyces albogriseolus

<400> 27

Lys Pro Phe Ile Ala Gly Gly Asp Ala Ile Thr Gly Asn Gly Gly Arg
 1 5 10 15
 Cys Ser Leu Gly Phe Asn Val Thr Lys Gly Gly Glu Pro His Phe Leu
 20 25 30
 Thr Ala Gly His Cys Thr Glu Gly Ile Ser Thr Trp Ser Asp Ser Ser

<400> 29

Thr	Pro	Leu	Ile	Ala	Gly	Gly	Asp	Ala	Ile	Trp	Gly	Ser	Gly	Ser	Arg
1				5					10					15	
Cys	Ser	Leu	Gly	Phe	Asn	Val	Val	Lys	Gly	Gly	Glu	Pro	Tyr	Phe	Leu
		20						25					30		
Thr	Ala	Gly	His	Cys	Thr	Glu	Ser	Val	Thr	Ser	Trp	Ser	Asp	Thr	Gln
		35						40					45		
Gly	Gly	Ser	Glu	Ile	Gly	Ala	Asn	Glu	Gly	Ser	Ser	Phe	Pro	Glu	Asn
	50					55					60				
Asp	Tyr	Gly	Leu	Val	Lys	Tyr	Thr	Ser	Asp	Thr	Ala	His	Pro	Ser	Glu
65					70					75					80
Val	Asn	Leu	Tyr	Asp	Gly	Ser	Thr	Gln	Ala	Ile	Thr	Gln	Ala	Gly	Asp
				85					90					95	
Ala	Thr	Val	Gly	Gln	Ala	Val	Thr	Arg	Ser	Gly	Ser	Thr	Thr	Gln	Val
		100						105						110	
His	Asp	Gly	Glu	Val	Thr	Ala	Leu	Asp	Ala	Thr	Val	Asn	Tyr	Gly	Asn
	115						120					125			
Gly	Asp	Ile	Val	Asn	Gly	Leu	Ile	Gln	Thr	Thr	Val	Cys	Ala	Glu	Pro
	130					135					140				
Gly	Asp	Ser	Gly	Gly	Ala	Leu	Phe	Ala	Gly	Asp	Thr	Ala	Leu	Gly	Leu
145					150					155					160
Thr	Ser	Gly	Gly	Ser	Gly	Asp	Cys	Ser	Ser	Gly	Gly	Thr	Thr	Phe	Phe
				165					170					175	
Gln	Pro	Val	Pro	Glu	Ala	Leu	Ala	Ala	Tyr	Gly	Ala	Glu	Ile	Gly	
		180						185						190	

<210> 30

<211> 200

<212> PRT

<213> Streptomyces lividans

<400> 30

Lys	Thr	Phe	Ala	Ser	Gly	Gly	Asp	Ala	Ile	Phe	Gly	Gly	Gly	Ala	Arg
1				5					10					15	
Cys	Ser	Leu	Gly	Phe	Asn	Val	Thr	Ala	Gly	Asp	Gly	Ser	Ala	Ala	Phe
		20						25					30		
Leu	Thr	Arg	Gly	His	Cys	Gly	Gly	Gly	Ala	Thr	Met	Trp	Ser	Asp	Ala
		35					40					45			
Gln	Gly	Gly	Gln	Pro	Ile	Ala	Thr	Val	Asp	Gln	Ala	Val	Phe	Pro	Pro
	50					55					60				
Glu	Gly	Asp	Phe	Gly	Leu	Val	Arg	Tyr	Asp	Gly	Pro	Ser	Thr	Glu	Ala
65					70					75					80
Pro	Ser	Glu	Val	Asp	Leu	Gly	Asp	Gln	Thr	Leu	Pro	Ile	Ser	Gly	Ala
				85					90					95	
Ala	Glu	Ala	Ser	Val	Gly	Gln	Glu	Val	Phe	Arg	Met	Gly	Ser	Thr	Thr
		100						105						110	
Gly	Leu	Ala	Asp	Gly	Gln	Val	Leu	Gly	Leu	Asp	Val	Thr	Val	Asn	Tyr
		115					120					125			
Pro	Glu	Gly	Thr	Val	Thr	Gly	Leu	Ile	Gln	Thr	Asp	Val	Cys	Ala	Glu
	130					135					140				
Pro	Gly	Asp	Ser	Gly	Gly	Ser	Leu	Phe	Thr	Arg	Asp	Gly	Leu	Ala	Ile
145					150					155					160
Arg	Leu	Thr	Ser	Gly	Gly	Thr	Arg	Asp	Cys	Thr	Ser	Gly	Gly	Glu	Thr
				165					170					175	
Phe	Phe	Gln	Pro	Val	Thr	Thr	Ala	Leu	Ala	Ala	Val	Gly	Gly	Thr	Leu

	180		185		190
Gly Gly Glu Asp Gly Gly Asp Gly					
	195		200		

<210> 31
 <211> 201
 <212> PRT
 <213> Streptomyces coelicolor

<400> 31

Lys Thr Phe Ala Ser Gly Gly Asp Ala Ile Phe Gly Gly Gly Ala Arg					
1	5		10		15
Cys Ser Leu Gly Phe Asn Val Thr Ala Gly Asp Gly Ser Pro Ala Phe					
	20		25		30
Leu Thr Ala Gly His Cys Gly Val Ala Ala Asp Gln Trp Ser Asp Ala					
	35		40		45
Gln Gly Gly Gln Pro Ile Ala Thr Val Asp Gln Ala Val Phe Pro Gly					
	50		55		60
Glu Gly Asp Phe Ala Leu Val Arg Tyr Asp Asp Pro Ala Thr Glu Ala					
65		70		75	80
Pro Ser Glu Val Asp Leu Gly Asp Gln Thr Leu Pro Ile Ser Gly Ala					
	85		90		95
Ala Glu Ala Ala Val Gly Gln Glu Val Phe Arg Met Gly Ser Thr Thr					
	100		105		110
Gly Leu Ala Asp Gly Gln Val Leu Gly Leu Asp Ala Thr Val Asn Tyr					
	115		120		125
Pro Glu Gly Met Val Thr Gly Leu Ile Gln Thr Asp Val Cys Ala Glu					
	130		135		140
Pro Gly Asp Ser Gly Gly Ser Leu Phe Thr Arg Asp Gly Leu Ala Ile					
145		150		155	160
Gly Leu Thr Ser Gly Gly Ser Gly Asp Cys Thr Val Gly Gly Glu Thr					
	165		170		175
Phe Phe Gln Pro Val Thr Thr Ala Leu Ala Ala Val Gly Ala Thr Leu					
	180		185		190
Gly Gly Glu Asp Gly Gly Ala Gly Ala					
	195		200		

<210> 32
 <211> 68
 <212> PRT
 <213> Streptomyces platensis

<400> 32

Val Asp Gly Leu Ile Gln Thr Asp Val Cys Ala Glu Pro Gly Asp Ser					
1	5		10		15
Gly Gly Ala Leu Phe Asp Gly Asp Ala Ala Ile Gly Leu Thr Ser Gly					
	20		25		30
Gly Ser Gly Asp Cys Ser Gln Gly Glu Thr Phe Phe Gln Pro Val					
	35		40		45
Thr Glu Ala Leu Lys Ala Tyr Gly Ala Gln Ile Gly Gly Gly Gln Gly					
	50		55		60
Glu Pro Pro Glu					
65					

<210> 33

<211> 201
 <212> PRT
 <213> Streptomyces coelicolor

<400> 33

Thr	Thr	Arg	Leu	Asn	Gly	Ala	Glu	Pro	Ile	Leu	Ser	Thr	Ala	Gly	Arg
1			5					10						15	
Cys	Ser	Ala	Gly	Phe	Asn	Val	Thr	Asp	Gly	Thr	Ser	Asp	Phe	Ile	Leu
		20						25					30		
Thr	Ala	Gly	His	Cys	Gly	Pro	Thr	Gly	Ser	Val	Trp	Phe	Gly	Asp	Arg
	35						40					45			
Pro	Gly	Asp	Gly	Gln	Val	Gly	Arg	Thr	Val	Ala	Gly	Ser	Phe	Pro	Gly
	50					55					60				
Asp	Asp	Phe	Ser	Leu	Val	Glu	Tyr	Ala	Asn	Gly	Lys	Ala	Gly	Asp	Gly
65				70					75					80	
Ala	Asp	Val	Val	Ala	Val	Gly	Asp	Gly	Lys	Gly	Val	Arg	Ile	Thr	Gly
			85					90						95	
Ala	Gly	Glu	Pro	Ala	Val	Gly	Gln	Arg	Val	Phe	Arg	Ser	Gly	Ser	Thr
			100					105					110		
Ser	Gly	Leu	Arg	Asp	Gly	Arg	Val	Thr	Ala	Leu	Asp	Ala	Thr	Val	Asn
	115						120					125			
Tyr	Pro	Glu	Gly	Thr	Val	Thr	Gly	Leu	Ile	Glu	Thr	Asp	Val	Cys	Ala
	130					135					140				
Glu	Pro	Gly	Asp	Ser	Gly	Gly	Pro	Met	Phe	Ser	Glu	Gly	Val	Ala	Leu
145					150					155				160	
Gly	Val	Thr	Ser	Gly	Gly	Ser	Gly	Asp	Cys	Ala	Lys	Gly	Gly	Thr	Thr
			165					170						175	
Phe	Phe	Gln	Pro	Leu	Pro	Glu	Ala	Met	Ala	Ser	Leu	Gly	Val	Arg	Leu
			180					185					190		
Ile	Val	Pro	Gly	Arg	Glu	Gly	Ala	Ala							
	195						200								

<210> 34
 <211> 188
 <212> PRT
 <213> Metarhizium anisopliae

<400> 34

Ala	Thr	Val	Gln	Gly	Gly	Asp	Val	Tyr	Tyr	Ile	Asn	Arg	Ser	Ser	Arg
1			5					10						15	
Cys	Ser	Ile	Gly	Phe	Ala	Val	Thr	Thr	Gly	Phe	Val	Ser	Ala	Gly	His
		20						25					30		
Cys	Gly	Gly	Ser	Gly	Ala	Ser	Ala	Thr	Thr	Ser	Ser	Gly	Glu	Ala	Leu
	35						40					45			
Gly	Thr	Phe	Ser	Gly	Ser	Val	Phe	Pro	Gly	Ser	Ala	Asp	Met	Ala	Tyr
	50					55					60				
Val	Arg	Thr	Val	Ser	Gly	Thr	Val	Leu	Arg	Gly	Tyr	Ile	Asn	Gly	Tyr
65				70					75					80	
Gly	Gln	Gly	Ser	Phe	Pro	Val	Ser	Gly	Ser	Ser	Glu	Ala	Ala	Val	Gly
			85					90						95	
Ala	Ser	Ile	Cys	Arg	Ser	Gly	Ser	Thr	Thr	Gln	Val	His	Cys	Gly	Thr
			100					105					110		
Ile	Gly	Ala	Lys	Gly	Ala	Thr	Val	Asn	Tyr	Pro	Gln	Gly	Ala	Val	Ser
	115						120					125			
Gly	Leu	Thr	Arg	Thr	Ser	Val	Cys	Ala	Glu	Pro	Gly	Asp	Ser	Gly	Gly

130		135		140
Ser Phe Tyr Ser Gly	Ser Gln Ala Gln Gly	Val Thr Ser Gly Gly Ser		
145	150	155	160	
Gly Asp Cys Ser Arg	Gly Gly Thr Thr Tyr Phe Gln Pro Val Asn Arg			
	165	170	175	
Ile Leu Gln Thr Tyr Gly Leu Thr Leu Val Thr Ala				
180	185			

<210> 35
 <211> 195
 <212> PRT
 <213> Streptomyces griseus

<400> 35

Ala Asp Ile Arg Gly Gly Asp Ala Tyr Tyr Met Asn Gly Ser Gly Arg		
1	5	10
Cys Ser Val Gly Phe Ser Val Thr Arg Gly Thr Gln Asn Gly Phe Ala		
	20	25
Thr Ala Gly His Cys Gly Arg Val Gly Thr Thr Thr Asn Gly Val Asn		
	35	40
Gln Gln Ala Gln Gly Thr Phe Gln Gly Ser Thr Phe Pro Gly Arg Asp		
	50	55
Ile Ala Trp Val Ala Thr Asn Ala Asn Trp Thr Pro Arg Pro Leu Val		
65	70	75
Asn Gly Tyr Gly Arg Gly Asp Val Thr Val Ala Gly Ser Thr Ala Ser		
	85	90
Val Val Gly Ala Ser Val Cys Arg Ser Gly Ser Thr Thr Gly Trp His		
	100	105
Cys Gly Thr Ile Gln Gln Leu Asn Thr Ser Val Thr Tyr Pro Glu Gly		
	115	120
Thr Ile Ser Gly Val Thr Arg Thr Ser Val Cys Ala Glu Pro Gly Asp		
	130	135
Ser Gly Gly Ser Tyr Ile Ser Gly Ser Gln Ala Gln Gly Val Thr Ser		
145	150	155
Gly Gly Ser Gly Asn Cys Ser Ser Gly Gly Thr Thr Tyr Phe Gln Pro		
	165	170
Ile Asn Pro Leu Leu Gln Ala Tyr Gly Leu Thr Leu Val Thr Ser Gly		
	180	185
Gly Gly Thr		190
195		

<210> 36
 <211> 197
 <212> PRT
 <213> Streptomyces coelicolor

<400> 36

Tyr Asp Leu Arg Gly Gly Glu Ala Tyr Tyr Ile Asn Asn Ser Ser Arg		
1	5	10
Cys Ser Ile Gly Phe Pro Ile Thr Lys Gly Thr Gln Gln Gly Phe Ala		
	20	25
Thr Ala Gly His Cys Gly Arg Ala Gly Ser Ser Thr Thr Gly Ala Asn		
	35	40
Arg Val Ala Gln Gly Thr Phe Gln Gly Ser Ile Phe Pro Gly Arg Asp		
	50	55
		60

Met	Ala	Trp	Val	Ala	Thr	Asn	Ser	Ser	Trp	Thr	Ala	Thr	Pro	Tyr	Val
65					70					75				80	
Leu	Gly	Ala	Gly	Gly	Gln	Asn	Val	Gln	Val	Thr	Gly	Ser	Thr	Ala	Ser
			85						90					95	
Pro	Val	Gly	Ala	Ser	Val	Cys	Arg	Ser	Gly	Ser	Thr	Thr	Gly	Trp	His
		100						105					110		
Cys	Gly	Thr	Val	Thr	Gln	Leu	Asn	Thr	Ser	Val	Thr	Tyr	Gln	Glu	Gly
	115						120					125			
Thr	Ile	Ser	Pro	Val	Thr	Arg	Thr	Thr	Val	Cys	Ala	Glu	Pro	Gly	Asp
	130					135					140				
Ser	Gly	Gly	Ser	Phe	Ile	Ser	Gly	Ser	Gln	Ala	Gln	Gly	Val	Thr	Ser
145					150					155					160
Gly	Gly	Ser	Gly	Asp	Cys	Arg	Thr	Gly	Gly	Glu	Thr	Phe	Phe	Gln	Pro
			165					170						175	
Ile	Asn	Ala	Leu	Leu	Gln	Asn	Tyr	Gly	Leu	Thr	Leu	Lys	Thr	Thr	Gly
		180						185					190		
Gly	Asp	Asp	Gly	Gly											
	195														

<210> 37
 <211> 189
 <212> PRT
 <213> Streptomyces spp.

<400> 37

Tyr	Asp	Leu	Val	Gly	Gly	Asp	Ala	Tyr	Tyr	Ile	Gly	Asn	Gly	Arg	Cys
1			5						10					15	
Ser	Ile	Gly	Phe	Ser	Val	Arg	Gln	Gly	Ser	Thr	Pro	Gly	Phe	Val	Thr
		20						25					30		
Ala	Gly	His	Cys	Gly	Ser	Val	Gly	Asn	Ala	Thr	Thr	Gly	Phe	Asn	Arg
	35						40					45			
Val	Ser	Gln	Gly	Thr	Phe	Arg	Gly	Ser	Trp	Phe	Pro	Gly	Arg	Asp	Met
	50					55					60				
Ala	Trp	Val	Ala	Val	Asn	Ser	Asn	Trp	Thr	Pro	Thr	Ser	Leu	Val	Arg
65					70					75				80	
Asn	Ser	Gly	Ser	Gly	Val	Arg	Val	Thr	Gly	Ser	Thr	Gln	Ala	Thr	Val
			85						90					95	
Gly	Ser	Ser	Ile	Cys	Arg	Ser	Gly	Ser	Thr	Thr	Gly	Trp	Arg	Cys	Gly
		100						105					110		
Thr	Ile	Gln	Gln	His	Asn	Thr	Ser	Val	Thr	Tyr	Pro	Gln	Gly	Thr	Ile
	115						120					125			
Thr	Gly	Val	Thr	Arg	Thr	Ser	Ala	Cys	Ala	Gln	Pro	Gly	Asp	Ser	Gly
	130					135					140				
Gly	Ser	Phe	Ile	Ser	Gly	Thr	Gln	Ala	Gln	Gly	Val	Thr	Ser	Gly	Gly
145					150					155					160
Ser	Gly	Asn	Cys	Ser	Ile	Gly	Gly	Thr	Thr	Phe	His	Gln	Pro	Val	Asn
			165					170						175	
Pro	Ile	Leu	Ser	Gln	Tyr	Gly	Leu	Thr	Leu	Val	Arg	Ser			
		180						185							

<210> 38
 <211> 187
 <212> PRT
 <213> Streptomyces spp.

<400> 38

Tyr	Asp	Leu	Val	Gly	Gly	Asp	Ala	Tyr	Tyr	Met	Gly	Gly	Gly	Arg	Cys
1				5					10					15	
Ser	Val	Gly	Phe	Ser	Val	Thr	Gln	Gly	Ser	Thr	Pro	Gly	Phe	Ala	Thr
		20						25					30		
Ala	Gly	His	Cys	Gly	Thr	Val	Gly	Thr	Ser	Thr	Thr	Gly	Tyr	Asn	Gln
		35					40					45			
Ala	Ala	Gln	Gly	Thr	Phe	Glu	Glu	Ser	Ser	Phe	Pro	Gly	Asp	Asp	Met
	50					55					60				
Ala	Trp	Val	Ser	Val	Asn	Ser	Asp	Trp	Asn	Thr	Thr	Pro	Thr	Val	Asn
65					70					75					80
Glu	Gly	Glu	Val	Thr	Val	Ser	Gly	Ser	Thr	Glu	Ala	Ala	Val	Gly	Ala
				85					90					95	
Ser	Ile	Cys	Arg	Ser	Gly	Ser	Thr	Thr	Gly	Trp	His	Cys	Gly	Thr	Ile
			100					105					110		
Gln	Gln	His	Asn	Thr	Ser	Val	Thr	Tyr	Pro	Glu	Gly	Thr	Ile	Thr	Gly
		115					120					125			
Val	Thr	Arg	Thr	Ser	Val	Cys	Ala	Glu	Pro	Gly	Asp	Ser	Gly	Gly	Ser
	130					135					140				
Tyr	Ile	Ser	Gly	Ser	Gln	Ala	Gln	Gly	Val	Thr	Ser	Gly	Gly	Ser	Gly
145					150					155					160
Asn	Cys	Thr	Ser	Gly	Gly	Thr	Thr	Tyr	His	Gln	Pro	Ile	Asn	Pro	Leu
				165				170					175		
Leu	Ser	Ala	Tyr	Gly	Leu	Asp	Leu	Val	Thr	Gly					
			180					185							

<210> 39

<211> 193

<212> PRT

<213> Streptomyces coelicolor

<400> 39

Glu	Asp	Leu	Val	Gly	Gly	Asp	Ala	Tyr	Tyr	Ile	Asp	Asp	Gln	Ala	Arg
1				5					10					15	
Cys	Ser	Ile	Gly	Phe	Ser	Val	Thr	Lys	Asp	Asp	Gln	Glu	Gly	Phe	Ala
		20						25					30		
Thr	Ala	Gly	His	Cys	Gly	Asp	Pro	Gly	Ala	Thr	Thr	Thr	Gly	Tyr	Asn
		35					40					45			
Glu	Ala	Asp	Gln	Gly	Thr	Phe	Gln	Ala	Ser	Thr	Phe	Pro	Gly	Lys	Asp
	50					55					60				
Met	Ala	Trp	Val	Gly	Val	Asn	Ser	Asp	Trp	Thr	Ala	Thr	Pro	Asp	Val
65					70					75					80
Lys	Ala	Glu	Gly	Gly	Glu	Lys	Ile	Gln	Leu	Ala	Gly	Ser	Val	Glu	Ala
			85					90					95		
Leu	Val	Gly	Ala	Ser	Val	Cys	Arg	Ser	Gly	Ser	Thr	Thr	Gly	Trp	His
		100						105					110		
Cys	Gly	Thr	Ile	Gln	Gln	His	Asp	Thr	Ser	Val	Thr	Tyr	Pro	Glu	Gly
		115					120					125			
Thr	Val	Asp	Gly	Leu	Thr	Glu	Thr	Thr	Val	Cys	Ala	Glu	Pro	Gly	Asp
	130					135					140				
Ser	Gly	Gly	Pro	Phe	Val	Ser	Gly	Val	Gln	Ala	Gln	Gly	Thr	Thr	Ser
145					150					155					160
Gly	Gly	Ser	Gly	Asp	Cys	Thr	Asn	Gly	Gly	Thr	Thr	Phe	Tyr	Gln	Pro
				165				170					175		
Val	Asn	Pro	Leu	Leu	Ser	Asp	Phe	Gly	Leu	Thr	Leu	Lys	Thr	Thr	Ser
			180					185					190		

Ala

<210> 40
<211> 187
<212> PRT
<213> Thermobifida fusca

<400> 40

Leu	Ala	Ala	Ile	Ile	Gly	Gly	Asn	Pro	Tyr	Tyr	Phe	Gly	Asn	Tyr	Arg	
1				5					10					15		
Cys	Ser	Ile	Gly	Phe	Ser	Val	Arg	Gln	Gly	Ser	Gln	Thr	Gly	Phe	Ala	
			20					25					30			
Thr	Ala	Gly	His	Cys	Gly	Ser	Thr	Gly	Thr	Arg	Val	Ser	Ser	Pro	Ser	
		35					40					45				
Gly	Thr	Val	Ala	Gly	Ser	Tyr	Phe	Pro	Gly	Arg	Asp	Met	Gly	Trp	Val	
	50					55					60					
Arg	Ile	Thr	Ser	Ala	Asp	Thr	Val	Thr	Pro	Leu	Val	Asn	Arg	Tyr	Asn	
65					70					75				80		
Gly	Gly	Thr	Val	Thr	Val	Thr	Gly	Ser	Gln	Glu	Ala	Ala	Thr	Gly	Ser	
				85					90					95		
Ser	Val	Cys	Arg	Ser	Gly	Ala	Thr	Thr	Gly	Trp	Arg	Cys	Gly	Thr	Ile	
			100					105					110			
Gln	Ser	Lys	Asn	Gln	Thr	Val	Arg	Tyr	Ala	Glu	Gly	Thr	Val	Thr	Gly	
		115					120					125				
Leu	Thr	Arg	Thr	Thr	Ala	Cys	Ala	Glu	Gly	Gly	Asp	Ser	Gly	Gly	Pro	
	130					135					140					
Trp	Leu	Thr	Gly	Ser	Gln	Ala	Gln	Gly	Val	Thr	Ser	Gly	Gly	Thr	Gly	
145					150					155					160	
Asp	Cys	Arg	Ser	Gly	Gly	Ile	Thr	Phe	Phe	Gln	Pro	Ile	Asn	Pro	Leu	
				165					170					175		
Leu	Ser	Tyr	Phe	Gly	Leu	Gln	Leu	Val	Thr	Gly						
			180					185								

<210> 41
<211> 198
<212> PRT
<213> Lysobacter enzymogenes

<400> 41

Ala	Asn	Ile	Val	Gly	Gly	Ile	Glu	Tyr	Ser	Ile	Asn	Asn	Ala	Ser	Leu	
1				5					10					15		
Cys	Ser	Val	Gly	Phe	Ser	Val	Thr	Arg	Gly	Ala	Thr	Lys	Gly	Phe	Val	
			20					25					30			
Thr	Ala	Gly	His	Cys	Gly	Thr	Val	Asn	Ala	Thr	Ala	Arg	Ile	Gly	Gly	
		35					40					45				
Ala	Val	Val	Gly	Thr	Phe	Ala	Ala	Arg	Val	Phe	Pro	Gly	Asn	Asp	Arg	
	50					55					60					
Ala	Trp	Val	Ser	Leu	Thr	Ser	Ala	Gln	Thr	Leu	Leu	Pro	Arg	Val	Ala	
65					70					75				80		
Asn	Gly	Ser	Ser	Phe	Val	Thr	Val	Arg	Gly	Ser	Thr	Glu	Ala	Ala	Val	
				85					90					95		
Gly	Ala	Ala	Val	Cys	Arg	Ser	Gly	Arg	Thr	Thr	Gly	Tyr	Gln	Cys	Gly	
			100					105					110			
Thr	Ile	Thr	Ala	Lys	Asn	Val	Thr	Ala	Asn	Tyr	Ala	Glu	Gly	Ala	Val	

	115		120		125
Arg Gly	Leu Thr Gln Gly	Asn Ala Cys Met Gly	Arg Gly Asp Ser Gly		
130		135	140		
Gly Ser Trp	Ile Thr Ser Ala Gly	Gln Ala Gln Gly	Val Met Ser Gly		
145		150	155		160
Gly Asn Val	Gln Ser Asn Gly	Asn Asn Cys Gly	Ile Pro Ala Ser Gln		
	165	170	175		
Arg Ser Ser	Leu Phe Glu Arg Leu	Gln Pro Ile Leu Ser	Gln Tyr Gly		
	180	185	190		
Leu Ser Leu	Val Thr Gly				
	195				

<210> 42
 <211> 189
 <212> PRT
 <213> Streptomyces coelicolor

<400> 42

Ala Ala Gly	Thr Val Gly Gly	Asp Pro Tyr Tyr	Thr Gly Asn Val Arg		
1	5	10	15		
Cys Ser Ile	Gly Phe Ser Val His	Gly Gly Phe Val Thr	Ala Gly His		
	20	25	30		
Cys Gly Arg	Ala Gly Ala Gly	Val Ser Gly Trp Asp	Arg Ser Tyr Ile		
	35	40	45		
Gly Thr Phe	Gln Gly Ser Ser	Phe Pro Asp Asn Asp	Tyr Ala Trp Val		
	50	55	60		
Ser Val Gly	Ser Gly Trp Trp	Thr Val Pro Val Val	Leu Gly Trp Gly		
	65	70	75	80	
Thr Val Ser	Asp Gln Leu Val Arg	Gly Ser Asn Val Ala	Pro Val Gly		
	85	90	95		
Ala Ser Ile	Cys Arg Ser Gly Ser	Thr Thr His Trp His	Cys Gly Thr		
	100	105	110		
Val Leu Ala	His Asn Glu Thr Val	Asn Tyr Ser Asp Gly	Ser Val Val		
	115	120	125		
His Gln Leu	Thr Lys Thr Ser Val	Cys Ala Glu Gly Gly	Asp Ser Gly		
	130	135	140		
Gly Ser Phe	Ile Ser Gly Asp Gln	Ala Gln Gly Val Thr	Ser Gly Gly		
	145	150	155	160	
Trp Gly Asn	Cys Ser Ser Gly Gly	Glu Thr Trp Phe Gln	Pro Val Asn		
	165	170	175		
Glu Ile Leu	Asn Arg Tyr Gly Leu	Thr Leu His Thr Ala			
	180	185			

<210> 43
 <211> 197
 <212> PRT
 <213> Rarobacter faecitabidus

<400> 43

Val Ile Val	Pro Val Arg Asp Tyr	Trp Gly Gly Asp	Ala Leu Ser Gly		
1	5	10	15		
Cys Thr Leu	Ala Phe Pro Val Tyr	Gly Gly Phe Leu Thr	Ala Gly His		
	20	25	30		
Cys Ala Val	Glu Gly Lys Gly His	Ile Leu Lys Thr Glu	Met Thr Gly		
	35	40	45		

Gly	Gln	Ile	Gly	Thr	Val	Glu	Ala	Ser	Gln	Phe	Gly	Asp	Gly	Ile	Asp
50						55					60				
Ala	Ala	Trp	Ala	Lys	Asn	Tyr	Gly	Asp	Trp	Asn	Gly	Arg	Gly	Arg	Val
65					70					75					80
Thr	His	Trp	Asn	Gly	Gly	Gly	Gly	Val	Asp	Ile	Lys	Gly	Ser	Asn	Glu
			85						90					95	
Ala	Ala	Val	Gly	Ala	His	Met	Cys	Lys	Ser	Gly	Arg	Thr	Thr	Lys	Trp
		100						105						110	
Thr	Cys	Gly	Tyr	Leu	Leu	Arg	Lys	Asp	Val	Ser	Val	Asn	Tyr	Gly	Asn
		115					120					125			
Gly	His	Ile	Val	Thr	Leu	Asn	Glu	Thr	Ser	Ala	Cys	Ala	Leu	Gly	Gly
		130				135					140				
Asp	Ser	Gly	Gly	Ala	Tyr	Val	Trp	Asn	Asp	Gln	Ala	Gln	Gly	Ile	Thr
145					150					155					160
Ser	Gly	Ser	Asn	Met	Asp	Thr	Asn	Asn	Cys	Arg	Ser	Phe	Tyr	Gln	Pro
			165						170					175	
Val	Asn	Thr	Val	Leu	Asn	Lys	Trp	Lys	Leu	Ser	Leu	Val	Thr	Ser	Thr
			180					185					190		
Asp	Val	Thr	Thr	Ser											
			195												

<210> 44
 <211> 191
 <212> PRT
 <213> Streptomyces coelicolor

<400> 44

Asp	Pro	Pro	Leu	Arg	Ser	Gly	Leu	Ala	Ile	Tyr	Gly	Thr	Asn	Val	Arg
1			5						10					15	
Cys	Ser	Ser	Ala	Phe	Met	Ala	Tyr	Ser	Gly	Ser	Ser	Tyr	Tyr	Met	Met
			20					25					30		
Thr	Ala	Gly	His	Cys	Ala	Glu	Asp	Ser	Ser	Tyr	Trp	Glu	Val	Pro	Thr
		35					40					45			
Tyr	Ser	Tyr	Gly	Tyr	Gln	Gly	Val	Gly	His	Val	Ala	Asp	Tyr	Thr	Phe
	50					55				60					
Gly	Tyr	Tyr	Gly	Asp	Ser	Ala	Ile	Val	Arg	Val	Asp	Asp	Pro	Gly	Phe
65					70				75						80
Trp	Gln	Pro	Arg	Gly	Trp	Val	Tyr	Pro	Ser	Thr	Arg	Ile	Thr	Asn	Trp
			85					90					95		
Asp	Tyr	Asp	Tyr	Val	Gly	Gln	Tyr	Val	Cys	Lys	Gln	Gly	Ser	Thr	Thr
		100						105					110		
Gly	Tyr	Thr	Cys	Gly	Gln	Ile	Thr	Glu	Thr	Asn	Ala	Thr	Val	Ser	Tyr
		115					120						125		
Pro	Gly	Arg	Thr	Leu	Thr	Gly	Met	Thr	Trp	Ser	Thr	Ala	Cys	Asp	Ala
	130					135					140				
Pro	Gly	Asp	Ser	Gly	Ser	Gly	Val	Tyr	Asp	Gly	Ser	Thr	Ala	His	Gly
145					150					155					160
Ile	Leu	Ser	Gly	Gly	Pro	Asn	Ser	Gly	Cys	Gly	Met	Ile	His	Glu	Pro
			165					170					175		
Ile	Ser	Arg	Ala	Leu	Ala	Asp	Arg	Gly	Val	Thr	Leu	Leu	Ala	Gly	
			180					185					190		

<210> 45
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

 <400> 45
 tgcgccgagc ccggcgactc 20

 <210> 46
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> primer

 <400> 46
 gagtcgccgg gctcggcgca 20

 <210> 47
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> primer

 <400> 47
 ttccccggca acgactacgc gtgggt 26

 <210> 48
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> primer

 <400> 48
 acccacgcgt agtcgttgcc ggggaa 26

 <210> 49
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> primer

 <400> 49
 gccgctgctc gatcgggttc 20

 <210> 50
 <211> 24

 <212> DNA
 <213> Artificial Sequence

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<220>
<223> primer

<400> 50
gcagttgccg gagccgccgg acgt
24

<210> 51
<211> 14
<212> DNA
<213> Artificial Sequence

<220>

<223> synthetic

<220>
<221> misc_feature
<222> (7)..(7)
<223> n is a, c, g, or t

<400> 51
tsggsgncrt gggt
14

<210> 52
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 52

Leu Arg Met Ile Thr Thr Asp Ser Gly Ser Ser Pro
1 5 10

<210> 53
<211> 555
<212> DNA
<213> Cellulomonas flavigena

<400> 53
gtcgacgtca tcgggggcaa cgcgtactac atcgggtcgc gctcgcggtg ctcgatcggg 60
ttcgcggtcg agggcggggt cgtcaccgcg gggcactgcg ggcgcgcggg cgcgagcacg 120
tcgtcaccgt cggggacctt ccgcggctcg tcgttccccg gcaacgacta cgcgtgggtc 180
caggtcgcct cgggcaacac gccgcgcggg ctggtgaaca accactcggg cggcacggtg 240
cgcgtcaccg gctcgcagca ggccgcggtc ggctcgtacg tgtgccgatc gggcagcacg 300
acgggatggc ggtgcggcta cgtccgggcg tacaacacga ccgtgcggta cgcggagggc 360
tcggtctcgg gcctcatccg cacgagcgtg tgcgccgagc cgggcgactc cggcggctcg 420
ctggtcgccg gcacgcaggc ccagggcgtc acgtcgggcg ggtccggcaa ctgccgctac 480
gggggcacga cgtacttcca gcccgtgaac gagatcctgc aggaccagcc cgggcccgtc 540
accacgcgtg cccta
555

<210> 54
<211> 185

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<212> PRT
<213> Cellulomonas flavigena

<400> 54

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Val Asp Val Ile Gly Gly Asn Ala Tyr Tyr Ile Gly Ser Arg Ser Arg
1      5      10      15
Cys Ser Ile Gly Phe Ala Val Glu Gly Gly Phe Val Thr Ala Gly His
20      25      30
Cys Gly Arg Ala Gly Ala Ser Thr Ser Ser Pro Ser Gly Thr Phe Arg
35      40      45
Gly Ser Ser Phe Pro Gly Asn Asp Tyr Ala Trp Val Gln Val Ala Ser
50      55      60
Gly Asn Thr Pro Arg Gly Leu Val Asn Asn His Ser Gly Gly Thr Val
65      70      75      80
Arg Val Thr Gly Ser Gln Gln Ala Ala Val Gly Ser Tyr Val Cys Arg
85      90      95
Ser Gly Ser Thr Thr Gly Trp Arg Cys Gly Tyr Val Arg Ala Tyr Asn
100     105     110
Thr Thr Val Arg Tyr Ala Glu Gly Ser Val Ser Gly Leu Ile Arg Thr
115     120     125
Ser Val Cys Ala Glu Pro Gly Asp Ser Gly Gly Ser Leu Val Ala Gly
130     135     140
Thr Gln Ala Gln Gly Val Thr Ser Gly Gly Ser Gly Asn Cys Arg Tyr
145     150     155     160
Gly Gly Thr Thr Tyr Phe Gln Pro Val Asn Glu Ile Leu Gln Asp Gln
165     170     175
Pro Gly Pro Ser Thr Thr Arg Ala Leu
180     185
```

<210> 55
<211> 1009
<212> DNA
<213> Cellulomonas biazotea

<400> 55

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taaaacagac ggccagtga tttgtaatac gactcactat aggcgaattg aatttagcgg 60
ccgcgaattc gcccttacct atagggcacg cgtggtcgac ggccctgggc tggtagctcg 120
acgtcactac caacacgggc gtcgtcaacg ccaccgccct cgccgtggcc caggcgaccg 180
agatcgtcgc cgccgcaacg gtgcccgcgc acgcggtccg ggtcgtcgag accaccgagg 240
cgccccgcac gttcatcgac gtcatcggcg gcaaccgtta ccggatcaac aacacctcgc 300
gctgctcggc cggttcgcgc gtcagcggcg gcttcgtcac cgccgggcac tgcggcacga 360
ccggcgcgac cagcagaaa ccgtccggca cgttcgccgg ctcgtcggtc cccggcaacg 420
actacgcgtg ggtgcgcgtc gcgtccggca acaccccggt cggcgcgtg aacaactaca 480
gcggcggcac cgtggccgct gccggctcga cgcaggcgac cgtcggtgcg tccgtctgcc 540
gctccggctc caccacgggg tggcgctgcg ggacgatcca ggcgttcaac tccaccgtca 600
actacgcgca gggcagcgtc tccggcctca tccgcacgaa cgtgtgcgcc gagcccggcg 660
actccggcgg ctcgctcatc gccggcaacc aggccaggcg cctgacgtcc ggcgggtcgg 720
gcaactgcac caccggcggg acgacgtact tccagcccggt caacgaggcg ctctccgcct 780
acggcctgac gtcgtcacg tcgtccggcg gcggcggtgg cggcggcacg acctgcaccg 840
ggtacgcgcg gacctacacc ggctcgctcg cctcgcgggc gtcgcgcgtc cagccgtccg 900
gcagctatgt gaccgtcggg tccagcggca ccatccgcgt ctgcctcgac ggcccagagcg 960
ggacggactt cgacctgtac ctgcagaagt ggaacggggt cgcgtggggc 1009
```

<210> 56
<211> 335
<212> PRT

<213> Cellulomonas biazotea

<400> 56

Lys Gln Thr Ala Ser Glu Phe Val Ile Arg Leu Thr Ile Gly Glu Leu
1 5 10 15
Asn Leu Ala Ala Asn Ser Pro Leu Pro Ile Gly His Ala Trp Ser
20 25 30
Thr Ala Leu Gly Trp Tyr Val Asp Val Thr Thr Asn Thr Val Val Val
35 40 45
Asn Ala Thr Ala Leu Ala Val Ala Gln Ala Thr Glu Ile Val Ala Ala
50 55 60
Ala Thr Val Pro Ala Asp Ala Val Arg Val Val Glu Thr Thr Glu Ala
65 70 75 80
Pro Arg Thr Phe Ile Asp Val Ile Gly Gly Asn Arg Tyr Arg Ile Asn
85 90 95
Asn Thr Ser Arg Cys Ser Val Gly Phe Ala Val Ser Gly Gly Phe Val
100 105 110
Thr Ala Gly His Cys Gly Thr Thr Gly Ala Thr Thr Thr Lys Pro Ser
115 120 125
Gly Thr Phe Ala Gly Ser Ser Phe Pro Gly Asn Asp Tyr Ala Trp Val
130 135 140
Arg Val Ala Ser Gly Asn Thr Pro Val Gly Ala Val Asn Asn Tyr Ser
145 150 155 160
Gly Gly Thr Val Ala Val Ala Gly Ser Thr Gln Ala Thr Val Gly Ala
165 170 175
Ser Val Cys Arg Ser Gly Ser Thr Thr Gly Trp Arg Cys Gly Thr Ile
180 185 190
Gln Ala Phe Asn Ser Thr Val Asn Tyr Ala Gln Gly Ser Val Ser Gly
195 200 205
Leu Ile Arg Thr Asn Val Cys Ala Glu Pro Gly Asp Ser Gly Gly Ser
210 215 220
Leu Ile Ala Gly Asn Gln Ala Gln Gly Leu Thr Ser Gly Gly Ser Gly
225 230 235 240
Asn Cys Thr Thr Gly Gly Thr Thr Tyr Phe Gln Pro Val Asn Glu Ala
245 250 255
Leu Ser Ala Tyr Gly Leu Thr Leu Val Thr Ser Ser Gly Gly Gly Gly
260 265 270
Gly Gly Gly Thr Thr Cys Thr Gly Tyr Ala Arg Thr Tyr Thr Gly Ser
275 280 285
Leu Ala Ser Arg Gln Ser Ala Val Gln Pro Ser Gly Ser Tyr Val Thr
290 295 300
Val Gly Ser Ser Gly Thr Ile Arg Val Cys Leu Asp Gly Pro Ser Gly
305 310 315 320
Thr Asp Phe Asp Leu Tyr Leu Gln Lys Trp Asn Gly Ser Ala Trp
325 330 335

<210> 57

<211> 474

<212> DNA

<213> Cellulomonas fimi

<400> 57

gtggacgtga tcggcggcga cgcctactac atcggcggcc gcagccgctg ttcgatcggg 60
ttcgccgtca ccgggggctt cgtgaccgcc gggcactgcg gccgcaccgg cgcggccacg 120
acgagcccgt cgggcacgtt cgccggctcg agcttcccgg gcaacgacta cgcggtgggtg 180
cgggtcgcgt cgggcaacac gcccgtcggc gcggtgaaca actacagcgg cggcacggtc 240

gccgtcgccg gctcgaccca ggccgcccgtc ggtgcgaccg tgtgccgctc gggctccacc	300
accggctggc ggtgcgggcac catccaggcg ttcaacgcga ccgtcaacta cgccgagggc	360
agcgtctccg gcctcatccg cacgaacgtg tgcgccgagc cggcgactc gggcggctcg	420
ctcgtcgccg gcaaccaggc gcagggcatg acgtccggcg gctccgacaa ctgc	474

<210> 58
 <211> 144
 <212> PRT
 <213> Cellulomonas fimi

<400> 58

Val Asp Val Ile Gly Gly Asp Ala Tyr Tyr Ile Gly Gly Arg Ser Arg	
1 5 10 15	
Cys Ser Ile Gly Phe Ala Val Thr Gly Gly Phe Val Thr Ala Gly His	
20 25 30	
Cys Gly Arg Thr Gly Ala Ala Thr Thr Ser Pro Ser Gly Thr Phe Ala	
35 40 45	
Gly Ser Ser Phe Pro Gly Asn Asp Tyr Ala Trp Val Arg Val Ala Ser	
50 55 60	
Gly Asn Thr Pro Val Gly Ala Val Asn Asn Tyr Ser Gly Gly Thr Val	
65 70 75 80	
Ala Val Ala Gly Ser Thr Gln Ala Ala Val Gly Ala Thr Val Cys Arg	
85 90 95	
Ser Gly Ser Thr Thr Gly Trp Arg Cys Gly Thr Ile Gln Ala Phe Asn	
100 105 110	
Ala Thr Val Asn Tyr Ala Glu Gly Ser Val Ser Gly Leu Ile Arg Thr	
115 120 125	
Asn Val Cys Ala Glu Pro Gly Asp Ser Gly Gly Ser Leu Val Ala Gly	
130 135 140	

<210> 59
 <211> 462
 <212> DNA
 <213> Cellulomonas gelida

<400> 59	
ctcgcgggca accaggcgca gggcgtgacg tcggggcgggt cgggcaactg ctcgtcgggc	60
gggacgacgt acttcagcc cgtcaacgag gccctccggg tgtacgggct cacgctcgtg	120
acctctgacg gtgggggcac cgagccggcg ccgaccgggt gccagggcta tgcgcggacc	180
taccagggca gcgtctcggc cgggacgtcg gtcgcgcagc cgaacggttc gtacgtcacg	240
accggggggcg ggacgcaccg ggtgtgcctg agcggaccgg cgggcacgga cctggacctg	300
tacctgcaga agtggaaacgg gtactcgtgg gccagcgtcg cgcagtcgac gtcgcctggg	360
gccacggagg cggtcacgta caccgggacc gccggctact accgctacgt ggtccacgcg	420
tacgcggggt cgggggcgta caccctgggg gcgacgaccc cg	462

<210> 60
 <211> 154
 <212> PRT
 <213> Cellulomonas gelida

<400> 60	
Leu Ala Gly Asn Gln Ala Gln Gly Val Thr Ser Gly Gly Ser Gly Asn	
1 5 10 15	
Cys Ser Ser Gly Gly Thr Thr Tyr Phe Gln Pro Val Asn Glu Ala Leu	
20 25 30	
Arg Val Tyr Gly Leu Thr Leu Val Thr Ser Asp Gly Gly Gly Thr Glu	

aagctcgtcg	tcgagtcggt	cggcgacacc	gcggcgggccg	ccgacgccgt	cgccgccgcg	240
ggcctgcctg	ccgacgccgt	gacgctcgcg	accaccgagg	cgccacggac	gttcgtcgac	300
gtcatcggcg	gcaacgcgta	ctacatcaac	gcgagcagcc	gctgctcggg	cggcttcgcg	360
gtcgagggcg	ggttcgtcac	cgcggggccac	tgcggggcgcg	cgggcgcgag	cacgtcgtca	420
ccgtcgggga	ccttcgcgcg	ctcgtcgttc	cccggcaacg	actacgcgtg	ggtccaggtc	480
gcctcgggca	acacgccgcg	cgggctggtg	aacaaccact	cgggcggcac	ggtgcgcgtc	540
accggctcgc	agcaggccgc	ggtcggctcg	tacgtgtgcc	gatcgggcag	cacgacggga	600
tggcgggtgcg	gctacgtccg	ggcgtacaac	acgaccgtgc	ggtacgcgga	gggctcggtc	660
tcgggcctca	tccgcacgag	cgtgtgcgcc	gagccgggcg	actccggcgg	ctcgtcggtc	720
gccggcacgc	aggcccaggg	cgtcacgtcg	ggcgggtccg	gcaactgccg	ctacgggggc	780
acgacgtact	tccagcccgt	gaacgagatc	ctgcaggcct	acggtctgcg	tctcgtcctg	840
ggctgacacg	ctcgcggcgg	gccctcccct	gcccgctcgcg	cgccggcccc	accagcccgg	900
gccg						904

<210> 64
 <211> 300
 <212> PRT
 <213> Cellulomonas cellasea

<400> 64

Val	Gly	Arg	Val	Arg	Gln	Leu	Pro	Leu	Arg	Gly	His	Asp	Val	Leu	Pro
1			5					10					15		
Ala	Arg	Glu	Arg	Asp	Pro	Ala	Gly	Leu	Arg	Ser	Ala	Ser	Arg	Pro	Gly
		20					25					30			
Leu	Thr	Arg	Ser	Arg	Arg	Ala	Arg	Leu	Asp	Ala	Ala	Gly	Pro	Ser	Ala
	35					40					45				
Arg	Val	Ala	Ala	Trp	Tyr	Val	Asp	Val	Pro	Thr	Asn	Lys	Leu	Val	Val
	50				55						60				
Glu	Ser	Val	Gly	Asp	Thr	Ala	Ala	Ala	Ala	Asp	Ala	Val	Ala	Ala	Ala
65				70					75					80	
Gly	Leu	Pro	Ala	Asp	Ala	Val	Thr	Leu	Ala	Thr	Thr	Glu	Ala	Pro	Arg
			85					90					95		
Thr	Phe	Val	Asp	Val	Ile	Gly	Gly	Asn	Ala	Tyr	Tyr	Ile	Asn	Ala	Ser
		100						105					110		
Ser	Arg	Cys	Ser	Val	Gly	Phe	Ala	Val	Glu	Gly	Gly	Phe	Val	Thr	Ala
	115					120						125			
Gly	His	Cys	Gly	Arg	Ala	Gly	Ala	Ser	Thr	Ser	Ser	Pro	Ser	Gly	Thr
	130					135					140				
Phe	Arg	Gly	Ser	Ser	Phe	Pro	Gly	Asn	Asp	Tyr	Ala	Trp	Val	Gln	Val
145					150				155					160	
Ala	Ser	Gly	Asn	Thr	Pro	Arg	Gly	Leu	Val	Asn	Asn	His	Ser	Gly	Gly
			165					170					175		
Thr	Val	Arg	Val	Thr	Gly	Ser	Gln	Gln	Ala	Ala	Val	Gly	Ser	Tyr	Val
	180							185					190		
Cys	Arg	Ser	Gly	Ser	Thr	Thr	Gly	Trp	Arg	Cys	Gly	Tyr	Val	Arg	Ala
	195					200						205			
Tyr	Asn	Thr	Thr	Val	Arg	Tyr	Ala	Glu	Gly	Ser	Val	Ser	Gly	Leu	Ile
	210					215					220				
Arg	Thr	Ser	Val	Cys	Ala	Glu	Pro	Gly	Asp	Ser	Gly	Gly	Ser	Leu	Val
225				230					235					240	
Ala	Gly	Thr	Gln	Ala	Gln	Gly	Val	Thr	Ser	Gly	Gly	Ser	Gly	Asn	Cys
			245					250					255		
Arg	Tyr	Gly	Gly	Thr	Thr	Tyr	Phe	Gln	Pro	Val	Asn	Glu	Ile	Leu	Gln
	260						265					270			
Ala	Tyr	Gly	Leu	Arg	Leu	Val	Leu	Gly	His	Ala	Arg	Gly	Gly	Pro	Ser
	275					280						285			

Pro Ala Arg Arg Ala Pro Ala Pro Pro Ala Arg Ala
 290 295 300

<210> 65
 <211> 429
 <212> DNA
 <213> Cellulomonas xylanilytica

<400> 65
 cgctgctcga tcgggttcgc cgtgacgggc ggcttcgtga ccgccggcca ctgcggacgg 60
 tccggcgaga cgacgacgtc gccgagcggc acgttcgccg ggtccagctt tcccggcaac 120
 gactacgcct ggggtccgcgc ggcctcgggc aacacgccgg tcggtgcggt gaaccgctac 180
 gacggcagcc gggtgaccgt ggccgggtcc accgacgcgg ccgtcgggtgc cgcggctctgc 240
 cggtcggggg cgacgaccgc gtggggctgc ggcacgatcc agtcccgcgg cgcgagcgtc 300
 acgtacgcc agggcaccgt cagcgggctc atccgcacca acgtgtgcgc cgagccgggt 360
 gactccgggg ggtcgctgat cgcgggcacc caggcgcggg gcgtgacgtc cggcggctcc 420
 ggcaactgc 429

<210> 66
 <211> 143
 <212> PRT
 <213> Cellulomonas xylanilytica

<400> 66

Arg	Cys	Ser	Ile	Gly	Phe	Ala	Val	Thr	Gly	Gly	Phe	Val	Thr	Ala	Gly
1				5					10					15	
His	Cys	Gly	Arg	Ser	Gly	Ala	Thr	Thr	Ser	Pro	Ser	Gly	Thr	Phe	
			20					25				30			
Ala	Gly	Ser	Ser	Phe	Pro	Gly	Asn	Asp	Tyr	Ala	Trp	Val	Arg	Ala	Ala
			35				40					45			
Ser	Gly	Asn	Thr	Pro	Val	Gly	Ala	Val	Asn	Arg	Tyr	Asp	Gly	Ser	Arg
			50				55				60				
Val	Thr	Val	Ala	Gly	Ser	Thr	Asp	Ala	Ala	Val	Gly	Ala	Ala	Val	Cys
65					70				75					80	
Arg	Ser	Gly	Ser	Thr	Thr	Ala	Trp	Gly	Cys	Gly	Thr	Ile	Gln	Ser	Arg
				85				90						95	
Gly	Ala	Ser	Val	Thr	Tyr	Ala	Gln	Gly	Thr	Val	Ser	Gly	Leu	Ile	Arg
			100					105					110		
Thr	Asn	Val	Cys	Ala	Glu	Pro	Gly	Asp	Ser	Gly	Gly	Ser	Leu	Ile	Ala
			115				120					125			
Gly	Thr	Gln	Ala	Arg	Gly	Val	Thr	Ser	Gly	Gly	Ser	Gly	Asn	Cys	
			130				135						140		

<210> 67
 <211> 1284
 <212> DNA
 <213> Oerskovia turbata

<400> 67
 atggcacgat cattctggag gacgctcgcc acggcgtgcg ccgcgacggc actggttgcc 60
 ggccccgcag cgctcaccgc gaacgcgcgc acgcccaccc ccgacacccc gaccgtttca 120
 ccccagacct cctcgaaggt ctgcgccgag gtgctccgcg ccctccagcg ggacctgggg 180
 ctgagcgcca aggacgcgac gaagcgtctg gcgttccagt ccgacgcggc gagcaccgag 240
 gacgctctcg ccgacagcct ggacgcctac gcgggcgcct gggtcgaccc tgcgaggaac 300
 accctgtacg tcggcgctgc cgacagggcc gaggccaagg aggtccgttc ggccggagcg 360
 acccccgtgg tcgtcgacca cacgctcgcc gagctcgaca cgtggaaggc ggcgctcgac 420

ggtgagctca	acgaccccg	gggcgtccc	agctggttcg	tcgacgtcac	gaccaaccag	480
gtcgtcgtca	acgtgcacga	cggcggacgc	gccctcgcgg	agctggctgc	cgcgagcgcg	540
ggcgtgccc	ccgacgccat	cacctacgtg	acgacgaccg	aggctcctcg	tcccctcgtc	600
gacgtggtgg	gcggcaacgc	gtacaccatg	ggttcggggc	ggcgctgctc	ggtcggcttc	660
gcggtgaacg	ggggcttcat	cacggccggg	cactgcggct	cggtcggcac	ccgcacctcg	720
gggccggggc	gcacgttccg	ggggtcgaac	ttccccggca	acgactacgc	ctgggtgcag	780
gtcgcgcggg	gtaacacccc	ggtcggcgcg	gtcaacaact	acagcggtgg	gcgcgtcgcg	840
gtcgcagggg	cgacggccgc	gcccgtgggg	gcctcgggtc	gccggtcccg	ttccacgacg	900
ggctggcact	gcggcaccat	cggcgcgtac	aacacctcgg	tgacgtaccc	gcagggcacc	960
gtctcggggc	tcatccgcac	gaacgtgtgc	gccgagcccc	gcgactcggg	cggctcgcctc	1020
ctcgcgggca	accaggcgca	gggcgtgacc	tcgggcgggt	cgggcaactg	ctcgtcgggc	1080
gggacgacgt	acttccagcc	cgtcaacgag	gccctcgggg	ggtacgggct	cacgctcgtg	1140
acctctgacg	gtggggggccc	gagccgccgc	cgaccgggtg	ccagggctat	gcgcggacct	1200
accagggcag	cgtctcggcc	gggacgtcgg	tcgcgcagcg	aacggttcgt	acgtcacgac	1260
cgggggcggg	cgaccgggtg	tgcc				1284

<210> 68

<211> 428

<212> PRT

<213> Oerskovia turbata

<400> 68

Met	Ala	Arg	Ser	Phe	Trp	Arg	Thr	Leu	Ala	Thr	Ala	Cys	Ala	Ala	Thr
1			5					10					15		
Ala	Leu	Val	Ala	Gly	Pro	Ala	Ala	Leu	Thr	Ala	Asn	Ala	Ala	Thr	Pro
		20						25				30			
Thr	Pro	Asp	Thr	Pro	Thr	Val	Ser	Pro	Gln	Thr	Ser	Ser	Lys	Val	Ser
		35					40					45			
Pro	Glu	Val	Leu	Arg	Ala	Leu	Gln	Arg	Asp	Leu	Gly	Leu	Ser	Ala	Lys
	50					55				60					
Asp	Ala	Thr	Lys	Arg	Leu	Ala	Phe	Gln	Ser	Asp	Ala	Ala	Ser	Thr	Glu
65					70				75						80
Asp	Ala	Leu	Ala	Asp	Ser	Leu	Asp	Ala	Tyr	Ala	Gly	Ala	Trp	Val	Asp
			85					90						95	
Pro	Ala	Arg	Asn	Thr	Leu	Tyr	Val	Gly	Val	Ala	Asp	Arg	Ala	Glu	Ala
		100						105					110		
Lys	Glu	Val	Arg	Ser	Ala	Gly	Ala	Thr	Pro	Val	Val	Val	Asp	His	Thr
		115						120					125		
Leu	Ala	Glu	Leu	Asp	Thr	Trp	Lys	Ala	Ala	Leu	Asp	Gly	Glu	Leu	Asn
	130					135					140				
Asp	Pro	Ala	Gly	Val	Pro	Ser	Trp	Phe	Val	Asp	Val	Thr	Thr	Asn	Gln
145					150					155					160
Val	Val	Val	Asn	Val	His	Asp	Gly	Gly	Arg	Ala	Leu	Ala	Glu	Leu	Ala
			165					170						175	
Ala	Ala	Ser	Ala	Gly	Val	Pro	Ala	Asp	Ala	Ile	Thr	Tyr	Val	Thr	Thr
		180						185					190		
Thr	Glu	Ala	Pro	Arg	Pro	Leu	Val	Asp	Val	Val	Gly	Gly	Asn	Ala	Tyr
		195				200						205			
Thr	Met	Gly	Ser	Gly	Gly	Arg	Cys	Ser	Val	Gly	Phe	Ala	Val	Asn	Gly
	210					215					220				
Gly	Phe	Ile	Thr	Ala	Gly	His	Cys	Gly	Ser	Val	Gly	Thr	Arg	Thr	Ser
225					230					235					240
Gly	Pro	Gly	Gly	Thr	Phe	Arg	Gly	Ser	Asn	Phe	Pro	Gly	Asn	Asp	Tyr
			245					250					255		
Ala	Trp	Val	Gln	Val	Asp	Ala	Gly	Asn	Thr	Pro	Val	Gly	Ala	Val	Asn
		260						265					270		

Asn	Tyr	Ser	Gly	Gly	Arg	Val	Ala	Val	Ala	Gly	Ser	Thr	Ala	Ala	Pro
	275						280					285			
Val	Gly	Ala	Ser	Val	Cys	Arg	Ser	Gly	Ser	Thr	Thr	Gly	Trp	His	Cys
	290					295					300				
Gly	Thr	Ile	Gly	Ala	Tyr	Asn	Thr	Ser	Val	Thr	Tyr	Pro	Gln	Gly	Thr
305					310					315					320
Val	Ser	Gly	Leu	Ile	Arg	Thr	Asn	Val	Cys	Ala	Glu	Pro	Gly	Asp	Ser
			325						330					335	
Gly	Gly	Ser	Leu	Ala	Gly	Asn	Gln	Ala	Gln	Gly	Val	Thr	Ser	Gly	
		340					345					350			
Gly	Ser	Gly	Asn	Cys	Ser	Ser	Gly	Gly	Thr	Thr	Tyr	Phe	Gln	Pro	Val
	355						360					365			
Asn	Glu	Ala	Leu	Gly	Gly	Tyr	Gly	Leu	Thr	Leu	Val	Thr	Ser	Asp	Gly
	370					375					380				
Gly	Gly	Pro	Ser	Arg	Arg	Arg	Pro	Gly	Ala	Arg	Ala	Met	Arg	Gly	Pro
385					390					395					400
Thr	Arg	Ala	Ala	Ser	Arg	Pro	Gly	Arg	Arg	Ser	Arg	Ser	Glu	Arg	Phe
				405					410					415	
Val	Arg	His	Asp	Arg	Gly	Arg	Ala	Thr	Gly	Cys	Ala				
			420					425							

<210> 69
 <211> 524
 <212> DNA
 <213> Oerskovia jenensis

<400> 69	
gccgctgctc ggtcggcttc gcggtgaacg gcggttcgt caccgcaggc cactgcgggga	60
cggtgggcac ccgcacctcg gggccgggcg gcacgttcg cggtcgagc ttccccggca	120
acgactacgc ctgggtgcag gtcgacgcgg ggaacacccc ggtcggggcc gtcaacaact	180
acagcggtag acgcgtcgcg gtcgcgggct cgacggccgc acccgtgggt tcctcggctc	240
gccggtccgg ttccacgacg ggctggcgct gcggcacgat cgcggcctac aacagctcgg	300
tgacgtaccc gcaggggacc gtctccgggc tcatccgcac caacgtgtgc gccgagccgg	360
gcgactcggg cggtcgcctc ctgcggggca accaggcaca gggcctgacg tcgggcgggg	420
cgggcaactg ctgcgtcgggc ggcacgacgt acttcagcc cgtcaacgag gcgctctcgg	480
cctacggcct cacgctcgtg acctccggcg gcaggggcaa ctgc	524

<210> 70
 <211> 174
 <212> PRT
 <213> Oerskovia jenensis

<400> 70

Arg	Cys	Ser	Val	Gly	Phe	Ala	Val	Asn	Gly	Gly	Phe	Val	Thr	Ala	Gly
1			5					10					15		
His	Cys	Gly	Thr	Val	Gly	Thr	Arg	Thr	Ser	Gly	Pro	Gly	Gly	Thr	Phe
		20					25					30			
Arg	Gly	Ser	Ser	Phe	Pro	Gly	Asn	Asp	Tyr	Ala	Trp	Val	Gln	Val	Asp
		35				40					45				
Ala	Gly	Asn	Thr	Pro	Val	Gly	Ala	Val	Asn	Asn	Tyr	Ser	Gly	Gly	Arg
	50					55				60					
Val	Ala	Val	Ala	Gly	Ser	Thr	Ala	Ala	Pro	Val	Gly	Ser	Ser	Val	Cys
65					70				75					80	
Arg	Ser	Gly	Ser	Thr	Thr	Gly	Trp	Arg	Cys	Gly	Thr	Ile	Ala	Ala	Tyr
			85					90					95		
Asn	Ser	Ser	Val	Thr	Tyr	Pro	Gln	Gly	Thr	Val	Ser	Gly	Leu	Ile	Arg

100 105 110
 Thr Asn Val Cys Ala Glu Pro Gly Asp Ser Gly Gly Ser Leu Leu Ala

115 120 125
 Gly Asn Gln Ala Gln Gly Leu Thr Ser Gly Gly Ser Gly Asn Cys Ser
 130 135 140
 Ser Gly Gly Thr Thr Tyr Phe Gln Pro Val Asn Glu Ala Leu Ser Ala
 145 150 155 160
 Tyr Gly Leu Thr Leu Val Thr Ser Gly Gly Arg Gly Asn Cys
 165 170

<210> 71
 <211> 984
 <212> DNA
 <213> Cellulosimicrobium cellulans

<400> 71
 ccacgggaggc cgggtcgaggc agcgcgctcg tcgggctcgc gggcaagtgc atcgacgtcc 60
 ccgggtccga cttcagtgac ggcaagcgcc tccagctgtg gacgtgcaac gggtcgcagg 120
 cagcgctgga cgttcgaagc cgacggcacc gtacgcgcgg gcggcaagtgc catggacgtc 180
 gcgtggggcgc cgcggccgac ggcacggcgc tccagctcgc gaactgcacg gcaacgcggc 240
 ccagaagtgc gtgctcaacg gcgcggggcga cctcgtgtcg gtgctggcga acaaagtgcg 300
 tcgacgcgcgc cgggtgcgca ccgaggtact cgcggcgccg tacgagctca cggcgacgtg 360
 cgcggcgaggc accgctacat cacacgggac ccgggcgcgt cgtcgggctc ggcctgctcg 420
 atcgggtacg ccgtccaggg cggtctcgtc acggcggggc actgcggacg cggcgggaca 480
 aggagagtgc tcaccgcgag ctgggcgcgc atggggacgg tccaggcggc gtcgttcccc 540
 ggccacgact acgcgtgggt gcgcgtcgac gccgggttct cccccgtccc gcgggtgaac 600
 aactacgccg gcggcaccgt cgacgtcgcc ggctcggccg aggcgcccgt ggggtgcgtcg 660
 gtgtgcccgt cgggcgccac gaccggctgg cgctgcggcg tcatcgagca gaagaacatc 720
 accgtcaact acggcaacgg cgacgttccc ggcctcgtgc gcggcagcgc gtgcgcggag 780
 ggcggcgact cgggcggggt ggtgatctcc ggcaaccagg cgcagggcgt cacgtcgggc 840
 aggatcaacg actgctcgaa cggcgggcaag ttctcttacc agcccgatcg acggcctgtc 900
 gctcgtgacc acgggcggcg ggtcgggcag cgcgctcgtc gggctcgcgg gcaagtgcac 960
 cgacgtcccc ggggtccgact tcag 984

<210> 72
 <211> 328
 <212> PRT
 <213> Cellulosimicrobium cellulans

<400> 72
 Pro Arg Ala Ala Gly Arg Ala Ala Arg Ser Ser Gly Ser Arg Ala Ser
 1 5 10 15
 Ala Ser Thr Ser Pro Gly Pro Thr Ser Val Thr Ala Ser Ala Ser Ser
 20 25 30
 Cys Gly Arg Ala Thr Gly Arg Arg Gln Arg Trp Thr Phe Glu Ala Asp
 35 40 45
 Gly Thr Val Arg Ala Gly Gly Lys Cys Met Asp Val Ala Trp Ala Pro
 50 55 60
 Arg Pro Thr Ala Arg Arg Ser Ser Ser Arg Thr Ala Arg Gln Arg Gly
 65 70 75 80
 Pro Glu Val Arg Ala Gln Arg Arg Gly Arg Pro Arg Val Gly Ala Gly
 85 90 95
 Glu Gln Ser Ala Ser Thr Pro Pro Gly Ala His Arg Gly Thr Arg Gly

100	105	110
Ala Val Arg Ala His Gly Asp	Val Arg Gly Gly Asp	Arg Tyr Ile Thr
115	120	125
Arg Asp Pro Gly Ala Ser Ser	Gly Ser Ala Cys Ser	Ile Gly Tyr Ala
130	135	140
Val Gln Gly Gly Phe Val Thr	Ala Gly His Cys Gly	Arg Gly Gly Thr
145	150	155
Arg Arg Val Leu Thr Ala Ser	Trp Ala Arg Met Gly	Thr Val Gln Ala
165	170	175
Ala Ser Phe Pro Gly His Asp	Tyr Ala Trp Val Arg	Val Asp Ala Gly
180	185	190
Phe Ser Pro Val Pro Arg Val	Asn Asn Tyr Ala Gly	Gly Thr Val Asp
195	200	205
Val Ala Gly Ser Ala Glu Ala	Pro Val Gly Ala Ser	Val Cys Arg Ser
210	215	220
Gly Ala Thr Thr Gly Trp Arg	Cys Gly Val Ile Glu	Gln Lys Asn Ile
225	230	235
Thr Val Asn Tyr Gly Asn Gly	Asp Val Pro Gly Leu	Val Arg Gly Ser
245	250	255
Ala Cys Ala Glu Gly Gly Asp	Ser Gly Gly Ser Val	Ile Ser Gly Asn
260	265	270
Gln Ala Gln Gly Val Thr Ser	Gly Arg Ile Asn Asp	Cys Ser Asn Gly
275	280	285
Gly Lys Phe Leu Tyr Gln Pro	Asp Arg Arg Pro Val	Ala Arg Asp His
290	295	300
Gly Arg Arg Val Gly Gln Arg	Ala Arg Arg Ala Arg	Gly Gln Val His
305	310	315
Arg Arg Pro Arg Val Arg	Leu Gln	
325		

<210> 73
 <211> 257
 <212> DNA
 <213> Promicromonospora citrea

<400> 73	
ttccccggca acgactacgc gtgggtgaac acgggacacgg acgacaccct cgtcggcgcc	60
gtgaacaact acagcggcgg cacggtcaac gtcgcgggct cgaccgtgc cgccgtcggc	120
gcgacggtct gccgtcggg ctccacgacc ggctggcact gcggcaccat ccaggcgtg	180
aacgcgtcgg tcacctacgc cgagggcacc gtgagcggcc tcatccgcac caacgtgtgc	240
gccgagcccc gcgactc	257

<210> 74
 <211> 85
 <212> PRT
 <213> Promicromonospora citrea

<400> 74	
Phe Pro Gly Asn Asp Tyr Ala Trp Val Asn Thr Gly Thr Asp Asp Thr	
1 5 10 15	
Leu Val Gly Ala Val Asn Asn Tyr Ser Gly Gly Thr Val Asn Val Ala	
20 25 30	
Gly Ser Thr Arg Ala Ala Val Gly Ala Thr Val Cys Arg Ser Gly Ser	
35 40 45	
Thr Thr Gly Trp His Cys Gly Thr Ile Gln Ala Leu Asn Ala Ser Val	
50 55 60	

Thr Tyr Ala Glu Gly Thr Val Ser Gly Leu Ile Arg Thr Asn Val Cys
65 70 75 80
Ala Glu Pro Gly Asp
85

<210> 75
<211> 257
<212> DNA
<213> Promicromonospora sukumoe

<400> 75
ttccccggca acgactacgc gtgggtgaac gtcgggtccg acgacacccc gatcgggtgcg 60
gtcaacaact acagcggcgg caccgtgaac gtcgcgggct cgacccaggc cgccgtcggc 120
tccaccgtct gccgtccgg ttccacgacc ggctggcact gcggcaccat ccaggccttc 180
aacgcgtcgg tcacctacgc cgagggcacc gtgtccggcc tgatccgcac caacgtctgc 240
gccgagcccc gcgactc 257

<210> 76
<211> 85
<212> PRT
<213> Promicromonospora sukumoe

<400> 76

Phe Pro Gly Asn Asp Tyr Ala Trp Val Asn Val Gly Ser Asp Asp Thr
1 5 10 15
Pro Ile Gly Ala Val Asn Asn Tyr Ser Gly Gly Thr Val Asn Val Ala
20 25 30
Gly Ser Thr Gln Ala Ala Val Gly Ser Thr Val Cys Arg Ser Gly Ser
35 40 45
Thr Thr Gly Trp His Cys Gly Thr Ile Gln Ala Phe Asn Ala Ser Val
50 55 60
Thr Tyr Ala Glu Gly Thr Val Ser Gly Leu Ile Arg Thr Asn Val Cys
65 70 75 80
Ala Glu Pro Gly Asp
85

<210> 77
<211> 430
<212> DNA
<213> Xylanibacterium ulmi

<400> 77
gccgtgctc gatcgggttc gccgtgacgg gcgggttcgt gaccgccggc cactgcggac 60
ggtcgggcgc gacgacgacg tccgcgagcg gcacgttcgc cgggtccagc tttccccgca 120
acgactacgc ctgggtccgc gcggcctcgg gaacacgccg gtcgggtgcgg tgaaccgcta 180
cgacggcagc cgggtgaccg tggccgggtc caccgacgcg gccgtcggtg ccgcgggtctg 240
ccggtcgggg tcgacgaccg cgtggcgctg cggcagcagc cagtcccgcg gcgcgacggg 300
cacgtacgcc cagggcaccg tcagcgggct catccgcacc aacgtgtgcg ccgagccggg 360
tgactccggg gggtcgctga tcgcgggcac ccaggcgcag ggcgtgacgt ccggcgggctc 420
cggcaactgc 430

<210> 78
<211> 141
<212> PRT
<213> Xylanibacterium ulmi

<400> 78

Arg Cys Ser Ile Gly Phe Ala Val Thr Gly Gly Phe Val Thr Ala Gly
1 5 10 15
His Cys Gly Arg Ser Gly Ala Thr Thr Thr Ser Ala Ser Gly Thr Phe
20 25 30
Ala Gly Ser Ser Phe Pro Gly Asn Asp Tyr Ala Trp Val Arg Ala Ala
35 40 45
Ser Gly Asn Thr Pro Val Gly Ala Val Asn Arg Tyr Asp Gly Ser Arg
50 55 60
Val Thr Val Ala Gly Ser Thr Asp Ala Ala Val Gly Ala Ala Val Cys
65 70 75 80
Arg Ser Gly Ser Thr Thr Ala Trp Arg Cys Gly Thr Ile Gln Ser Arg
85 90 95
Gly Ala Thr Val Thr Tyr Ala Gln Gly Thr Val Ser Gly Leu Ile Arg
100 105 110
Thr Asn Val Cys Ala Glu Pro Gly Asp Ser Gly Gly Ser Leu Ile Ala
115 120 125
Gly Thr Gln Ala Gln Gly Val Thr Ser Gly Gly Ser Gly
130 135 140

<210> 79

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 79

accacgcgt agtcgttgcc

20

<210> 80

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 80

accacgcgt agtcgtdgcc gggg

24

<210> 81

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 81

tcgtcgtggt cgcgcggg

18

<210> 82

<211> 17

<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	primer	
<400>	82	
	cgacgtgctc gcgcccg	17
<210>	83	
<211>	18	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	primer	
<400>	83	
	cgcgcccagc tcgcggtg	18
<210>	84	
<211>	22	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	primer	
<400>	84	
	cggccccgag gtgcgggtgc cg	22
<210>	85	
<211>	22	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	primer	
<400>	85	
	cagcgtctcc ggcctcatcc gc	22
<210>	86	
<211>	22	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	primer	
<400>	86	
	ctcgggtctcg ggcctcatcc gc	22
<210>	87	
<211>	22	
<212>	DNA	
<213>	Artificial Sequence	

<220>
 <223> primer

 <400> 87
 cgacgttccc ggctcgtgc gc 22

 <210> 88
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> primer

 <400> 88
 caccgtctcg gggctcatcc gc 22

 <210> 89
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> primer

 <400> 89
 agcargtgt gcgccgagcc 20

 <210> 90
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> primer

 <400> 90
 ggcagcgcgt gcgcggaggg 20

 <210> 91
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> primer

 <400> 91
 gccgctgctc gatcgggttc 20

 <210> 92
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>

<223> primer

 <400> 92
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 <400> 93
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 <210> 94
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 <212> DNA
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 <220>
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 <400> 94
 ggcacgacgt acttccagcc cgtgaac 27

 <210> 95
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 <220>
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 <210> 97
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 <220>
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<210> 98
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<220>
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<400> 98
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<210> 99
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 <212> DNA
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<220>
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<400> 99
 caccacgag tagtcgtggc cggggaacga 30

<210> 100
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 <212> DNA
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<220>
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<400> 100
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<220>
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<210> 102
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<220>
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<210> 103
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 <210> 104
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 <220>
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 <211> 30
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<213> Artificial Sequence
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 <223> primer
 <400> 118
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 <210> 119
 <211> 36
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 <400> 119
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 <210> 120
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 <211> 18
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 <223> n is a, c, g, or t
 <400> 122
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<210> 123
<211> 27
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<220>
<223> primer

<400> 123
gtsgaygtsa tcggcggcga ygcstac

27

<210> 124
<211> 18
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<213> Artificial Sequence

<220>
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<220>
<221> misc_feature
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<223> n is a, c, g, or t

<400> 124
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18

<210> 125
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<213> Artificial Sequence

<220>
<223> consensus sequence

<220>
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<222> 1, 8-16, 24, 35, 36, 38, 39, 41-44, 48, 61-64, 66, 67, 69-71, 81, 87, 89, 93, 109-111, 113, 116
<223> Xaa can be any naturally occurring amino acid

<220>
<221> VARIANT
<222> 4, 19, 28, 108, 126
<223> Xaa is Ile or Val

<220>
<221> VARIANT
<222> 7, 157
<223> Xaa is Asn or Asp

<220>

<221> VARIANT
<222> 92, 99, 143
<223> Xaa is Ser or Ala

<220>
<221> VARIANT
<222> 112, 156
<223> Xaa is Asn or Gly

<220>
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<222> 21
<223> Xaa is Phe or Tyr

<220>
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<222> 40
<223> Xaa is Thr or Val

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<222> 59
<223> Xaa is Phe or Trp

<220>
<221> VARIANT
<222> 65
<223> Xaa is Gly or Asp

<220>
<221> VARIANT
<222> 68
<223> Xaa is Leu or Phe

<220>
<221> VARIANT
<222> 74
<223> Xaa is Asn or Arg

<220>
<221> VARIANT
<222> 75
<223> Xaa is Tyr or His

<220>
<221> VARIANT
<222> 76
<223> Xaa is Ser or Asp

<220>
<221> VARIANT
<222> 78
<223> Xaa is Gly or Ser

<220>
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<223> Xaa is Arg or Thr

<220>
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<222> 83
<223> Xaa is Ala or Thr

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<222> 85
<223> Xaa is His or Ser

<220>
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<222> 86
<223> Xaa is Thr or Gln

<220>
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<222> 102
<223> Xaa is Gly or Ala

<220>
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<222> 104
<223> Xaa is His or Arg

<220>
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<222> 107
<223> Xaa is Thr or Tyr

<220>
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<222> 114
<223> Xaa is Ser or Thr

<220>
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<222> 118
<223> Xaa is Pro or Ala

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<222> 119
<223> Xaa is Glu or Gln

<220>
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<222> 121
<223> Xaa is Thr, Ser, or Asp

<220>
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<222> 123
<223> Xaa is Arg or Ser

<220>
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<222> 128
<223> Xaa is Thr or Gly

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<222> 129
<223> Xaa is Thr, Asn, or Ser

<220>
<221> VARIANT
<222> 130
<223> Xaa is Val or Ala

<220>
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<222> 134
<223> Xaa is Pro or Gly

<220>
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<222> 141
<223> Xaa is Leu or Val

<220>
<221> VARIANT
<222> 142
<223> Xaa is Leu, Val, or Ile

<220>
<221> VARIANT
<222> 145
<223> Xaa is Asn or Thr

<220>
<221> VARIANT
<222> 148
<223> Xaa is Gln or Arg

<220>
<221> VARIANT
<222> 150
<223> Xaa is Val or Leu

<220>
<221> VARIANT
<222> 154
<223> Xaa is Gly or Arg

<220>
<221> VARIANT
<222> 155
<223> Xaa is Ser or Ile

<220>
<221> VARIANT
<222> 159, 160, 163-166, 169-189
<223> Xaa can be any naturally occurring amino acid

<400> 125

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1				5				10						15		
Cys	Ser	Xaa	Gly	Xaa	Ala	Val	Xaa	Gly	Gly	Phe	Xaa	Thr	Ala	Gly	His	
			20					25					30			
Cys	Gly	Xaa	Xaa	Gly	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Gly	Thr	Phe	Xaa	
		35					40					45				
Gly	Ser	Ser	Phe	Pro	Gly	Asn	Asp	Tyr	Ala	Xaa	Val	Xaa	Xaa	Xaa	Xaa	
	50					55					60					
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Val	Asn	Xaa	Xaa	Xaa	Gly	Xaa	Xaa	Val	
65					70				75						80	
Xaa	Val	Xaa	Gly	Xaa	Xaa	Xaa	Ala	Xaa	Val	Gly	Xaa	Xaa	Val	Cys	Arg	
			85						90					95		
Ser	Gly	Xaa	Thr	Thr	Xaa	Trp	Xaa	Cys	Gly	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	
		100						105					110			
Xaa	Xaa	Val	Xaa	Tyr	Xaa	Xaa	Gly	Xaa	Val	Xaa	Gly	Leu	Xaa	Arg	Xaa	
		115					120					125				
Xaa	Xaa	Cys	Ala	Glu	Xaa	Gly	Asp	Ser	Gly	Gly	Ser	Xaa	Xaa	Xaa	Gly	
		130				135					140					
Xaa	Gln	Ala	Xaa	Gly	Xaa	Thr	Ser	Gly	Xaa	Xaa	Xaa	Xaa	Cys	Xaa	Xaa	
145					150				155						160	
Gly	Gly	Xaa	Xaa	Xaa	Xaa	Gln	Pro	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	
			165					170						175		
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	
			180					185								

<210> 126
 <211> 16
 <212> PRT
 <213> Cellulomonas cellasea

<220>
 <221> VARIANT
 <222> (1)..(1)
 <223> Xaa is Ile or Tyr

<400> 126

Xaa	Ala	Trp	Asp	Ala	Phe	Ala	Glu	Asn	Val	Val	Asp	Trp	Ser	Ser	Arg
1				5					10					15	

<210> 127
 <211> 17
 <212> PRT
 <213> Cellulomonas cellasea

<400> 127

Tyr	Gly	Gly	Thr	Thr	Tyr	Phe	Gln	Pro	Val	Asn	Glu	Ile	Leu	Gln	Ala
1				5					10					15	

Tyr

<210> 128
 <211> 11
 <212> PRT
 <213> Cellulomonas flavigena

<220>
 <221> VARIANT
 <222> (4)..(11)
 <223> Xaa is Ile or Tyr

<400> 128

Val Asp Val Xaa Gly Gly Asn Ala Tyr Tyr Xaa
 1 5 10

<210> 129
 <211> 9
 <212> PRT
 <213> Cellulomonas fimi

<220>
 <221> VARIANT
 <222> (4)..(4)
 <223> Xaa is Ile or Tyr

<400> 129

Val Asp Val Xaa Gly Gly Asp Ala Tyr
 1 5

<210> 130
 <211> 305
 <212> DNA
 <213> Aspergillus niger

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 <222> (186)..(186)
 <223> n is a, c, g, or t

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 tggtaaggaa cgggggtcca cggggagaga gagatggcct tgacggtcct gggaagggga 180
 gcttcngcgc gggggaggat ggtcttgaga gagggggagc tagtaatgtc gtacttggac 240
 agggagtgtc ctttctccga cgcacagacc acctcagcgg agatggcatc gtgcagagac 300
 agacc 305

<210> 131
 <211> 1488
 <212> DNA
 <213> Cellulomonas strain 69B4

<400> 131
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 ccacgattag ctgaaaaact tgacctgac ttacttgaag caatggaacg cgatctgggg 180
 ttagatgcag aggaagcagc tgcaacgtta gcttttcagc atgacgcagc tgaaacggga 240
 gaggtctctt ctgaggaact cgacgaagat ttcgcgggca cgtgggttga agatgatgtg 300
 ctgtatgttg caaccactga tgaagatgct gttgaagaag tcgaaggcga aggagcaact 360
 gctgtgactg ttgagcattc tcttgctgat ttagaggcgt ggaagacggt tttggatgct 420

gcgctggagg	gtcatgatga	tgtgcctacg	tggtagctcg	acgtgcctac	gaattcggtg	480
gtcgttgctg	taaaggcagg	agcgcaggat	gtagctgcag	gacttgtgga	aggcgctgat	540
gtgccatcag	atgcggtcac	ttttgtagaa	acggacgaaa	cgcttagaac	gatgttcgac	600
gtaattggag	gcaacgcata	tactattggc	ggccgggtcta	gatgttctat	cggattcgca	660
gtaaacggtg	gcttcattac	tgccggtcac	tgcggaagaa	caggagccac	tactgccaat	720
ccgactggca	catttgcagg	tagctcgttt	ccgggaaatg	attatgcatt	cgtccgaaca	780
ggggcaggag	taaatttgct	tgcccaagtc	aataactact	cgggcggcag	agtccaagta	840
gcaggacata	cggccgcacc	agttggatct	gctgtatgcc	gctcaggtag	cactacaggt	900
tggcattgcg	gaactatcac	ggcgctgaat	tcgtctgtca	cgtatccaga	gggaacagtc	960
cgaggactta	tccgcacgac	ggtttgtgcc	gaaccagggtg	atagcggagg	tagcctttta	1020
gcgggaaatc	aagcccaagg	tgtcacgtca	ggtaggttctg	gaaattgtcg	gacgggggga	1080
acaacattct	ttcaaccagt	caacccgatt	ttgcaggctt	acggcctgag	aatgattacg	1140
actgactctg	gaagttcccc	tgctccagca	cctacatcat	gtacaggcta	cgcaagaacg	1200
ttcacaggaa	ccctcgcagc	aggaagagca	gcagctcaac	cgaacggtag	ctatgttcag	1260
gtcaaccgga	gcggtacaca	ttccgtctgt	ctcaatggac	ctagcgggtg	ggactttgat	1320
ttgtatgtgc	agcgatggaa	tggcagtagc	tgggtaaccg	tcgctcaatc	gacatcgccg	1380
ggaagcaatg	aaaccattac	gtaccgcgga	aatgctggat	attatcgcta	cgtgggttaac	1440
gctgcgtcag	gatcaggagc	ttacacaatg	ggactcacc	tcccctga		1488

<210> 132
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> linker

<400> 132

Asp Asp Asn Asp Pro Ile
 1 5

<210> 133
 <211> 1020
 <212> DNA
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<220>
 <223> synthetic

<400> 133

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ctaagtatta	gtaacggtga	attagtcaat	gaacgaggcg	aacaagttca	gttaaaaggg	180
atgagttccc	atggtttgca	atggtacggt	caatttgtaa	actatgaaag	catgaaatgg	240
ctaagagatg	attggggaat	aactgtattc	cgagcagcaa	tgtatacctc	ttcaggagga	300
tatattgacg	atccatcagt	aaaggaaaaa	gtaaaagaga	ctggttgaggc	tgcgatagac	360
cttggcata	atgtgatcat	tgattggcat	atccttttcag	acaatgaccc	gaatatatat	420
aaagaagaag	cgaaggattt	ctttgatgaa	atgtcagagt	tgtatggaga	ctatccgaat	480
gtgatatacg	aaattgcaaa	tgaaccgaat	ggtagtgatg	ttacgtggga	caatcaaata	540
aaaccgtatg	cagaagaagt	gattccgggt	attcgtgaca	atgaccctaa	taacattggt	600
attgtaggta	caggtagatg	gagtcaggat	gtccatcatg	cagccgataa	tcagcttgca	660
gacctaacg	tcatgtatgc	atttcatttt	tatgcaggaa	cacatggaca	aaattttacga	720
gaccaagtag	attatgcatt	agatcaagga	gcagcgatat	ttgttagtga	atggggggaca	780
agtgcagcta	cagggtgatg	tgggtgtgtt	ttagatgaag	cacaagtgtg	gattgacttt	840
atggatgaaa	gaaatttaag	ctgggccaac	tggctctctaa	cgcataagga	tgagtcatct	900
gcagcgtaa	tgccagggtg	aaatccaact	ggtaggttgg	cagaggctga	actatctcca	960

tctgggtacat ttgtgagggg aaaaataaga gaatcagcat ctgacaacaa tgatcccata 1020

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<211> 340
<212> PRT
<213> Artificial Sequence
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<400> 134

[illegible]

340

<210> 135
<211> 30
<212> PRT
<213> Cellulomonas strain 69B4

<400> 135

Met	Arg	Ser	Lys	Lys	Arg	Thr	Val	Thr	Arg	Ala	Leu	Ala	Val	Ala	Thr
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Ala	Ala	Ala	Thr	Leu	Leu	Ala	Gly	Gly	Met	Ala	Ala	Gln	Ala		
			20				25					30			

<210> 136
<211> 30
<212> PRT
<213> Cellulomonas strain 69B4

<400> 136

Met	Arg	Ser	Lys	Lys	Leu	Trp	Ile	Ser	Leu	Leu	Leu	Ala	Val	Ala	Thr
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Ala	Ala	Ala	Thr	Leu	Leu	Ala	Gly	Gly	Met	Ala	Ala	Gln	Ala		
			20				25					30			

<210> 137
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<212> DNA
<213> Artificial Sequence

<220>
<223> primer

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<210> 138
<211> 40
<212> DNA
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<220>
<223> primer

<400> 138
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40

<210> 139
<211> 40
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<220>
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ctagctaggt accatgacac cacgaactgt cacaagagct	40
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<211> 74
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 145
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<210> 146
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cagcagctgc taca 74

<210> 148
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gtgtgcaagc tttcaagggg aacttccaga gtcagtc 37

<210> 149
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<400> 149
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<210> 150
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 <212> DNA
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<220>
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<400> 150
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<210> 151
 <211> 48
 <212> DNA
 <213> Artificial Sequence

<220>
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<400> 151
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<210> 152
 <211> 36
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<220>
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Ala	Ala	Ala	Thr	Leu	Leu	Ala	Gly	Gly	Met	Ala	Ala	Gln	Ala	Asn	Glu
			20				25					30			
Pro	Ala	Pro	Pro	Gly	Ser	Ala	Ser	Ala	Pro	Pro	Arg	Leu	Ala	Glu	Lys
			35				40					45			
Leu	Asp	Pro	Asp	Leu	Leu	Glu	Ala	Met	Glu	Arg	Asp	Leu	Gly	Leu	Asp
	50				55				60						
Ala	Glu	Glu	Ala	Ala	Ala	Thr	Leu	Ala	Phe	Gln	His	Asp	Ala	Ala	Glu
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<210> 583

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 ccgtcctctg ttggggttasn nggaacttcc agagtcagt 39

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<220>
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<400> 595
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<210> 596
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<220>
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<210> 598
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 <220>
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 <400> 598
 atgattatgc attcgtctca acaggggcag gagtaaatt 38

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 <220>
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 <400> 599
 ataactactc gggcggcaca gtccaagtag caggacatac 40

 <210> 600
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 <220>
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 <400> 603
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 ttggcggccg gtctagatca tctatcggat tcgcagta 38

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 <400> 605
 tcattactgc cggtcactca ggaagaacag gagccact 38

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 <400> 607
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 <210> 608
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<212> DNA
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 <220>
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 <400> 608
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 <212> DNA
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 <220>
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 <400> 610
 tgcctcacat ttgtgccac 19

 <210> 611
 <211> 19
 <212> DNA
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 <220>
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 <400> 611
 caggatgtag ctgcaggac 19

 <210> 612
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 <220>
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 <400> 612
 ctcggttatg agttagttc 19

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<220>
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<400> 613
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 <212> DNA
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<220>
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<400> 614
 gcgtcctcca gaatgatcgt gccatgggta cctccggggg tctgtctctg 50

<210> 615
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 <212> DNA
 <213> Artificial Sequence

<220>
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<400> 615
 atccgctcgc ggatcccat tgtcagctcg ggcaccacc gtcagaggtc acgag 55

<210> 616
 <211> 42
 <212> DNA
 <213> Artificial Sequence

<220>
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<400> 616
 gcagcctgaa ctagttgcga tcctctagag atcgaacttc at 42

<210> 617
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 <212> DNA
 <213> Artificial Sequence

<220>
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<400> 617
 agaccgacga gacccgcgg accatgggctg acgtcatcgg cggcaacgcg tactac 56

<210> 618
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 <212> DNA
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<220>

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<400> 618
tcagccgatc cgctcgcgga tccccattgt cagcccagga cgagacgcag accgta 56

<210> 619
<211> 56
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 619
gtagtacgcg ttgccgccga tgacgtcgac catgggccgc ggggtctcgt cggctc 56

<210> 620
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 620
gcagcctgaa ctagttgcga tcctctagag atcgaacttc atgttcga 48

<210> 621
<211> 53
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 621
accgacgaga ccccgcgga catgcacggc gacgtgcgcg gcggcgaccg cta 53

<210> 622
<211> 53
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 622
tagcggtcgc cgccgcgcac gtcgccgtgc atgggccgcg ggggtctcgtc ggt 53

<210> 623
<211> 59
<212> DNA
<213> Artificial Sequence

<220>
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Ala Val Val Gly Thr Phe	Ala Ala Arg Val Phe	Pro Gly Asn Asp Arg
50	55	60
Ala Trp Val Ser Leu Thr	Ser Ala Gln Thr Leu	Leu Pro Arg Val Ala
65	70	75
Asn Gly Ser Ser Phe Val	Thr Val Arg Gly Ser	Thr Glu Ala Ala Val
85	90	95
Gly Ala Ala Val Cys Arg	Ser Gly Arg Thr Thr	Gly Tyr Gln Cys Gly
100	105	110
Thr Ile Thr Ala Lys Asn	Val Thr Ala Asn Tyr	Ala Glu Gly Ala Val
115	120	125
Arg Gly Leu Thr Gln Gly	Asn Ala Cys Met Gly	Arg Gly Asp Ser Gly
130	135	140
Gly Ser Trp Ile Thr Ser	Ala Gly Gln Ala Gln	Gly Val Met Ser Gly
145	150	155
Gly Asn Val Gln Ser Asn	Gly Asn Asn Cys Gly	Ile Pro Ala Ser Gln
165	170	175
Arg Ser Ser Leu Phe Glu	Arg Leu Gln Pro Ile	Leu Ser Gln Tyr Gly
180	185	190
Leu Ser Leu Val Thr Gly		
195		

<210> 628
 <211> 191
 <212> PRT
 <213> Streptomyces fradiae

<400> 628

Ile Ala Gly Gly Glu Ala	Ile Tyr Ala Ala Gly	Gly Gly Gly Arg Cys Ser
1	5	10
Leu Gly Phe Asn Val Arg	Ser Ser Ser Gly Ala	Thr Tyr Ala Leu Thr
20	25	30
Ala Gly His Cys Thr Glu	Ile Ala Ser Thr Trp	Tyr Thr Asn Ser Gly
35	40	45
Gln Thr Ser Leu Leu Gly	Thr Arg Ala Gly Thr	Ser Phe Pro Gly Asn
50	55	60
Asp Tyr Gly Leu Ile Arg	His Ser Asn Ala Ser	Ala Ala Asp Gly Arg
65	70	75
Val Tyr Leu Tyr Asn Gly	Ser Tyr Arg Asp Ile	Thr Gly Ala Gly Asn
85	90	95
Ala Tyr Val Gly Gln Thr	Val Gln Arg Ser Gly	Ser Thr Thr Gly Leu
100	105	110
His Ser Gly Arg Val Thr	Gly Leu Asn Ala Thr	Val Asn Tyr Gly Gly
115	120	125
Gly Asp Ile Val Ser Gly	Leu Ile Gln Thr Asn	Val Cys Ala Glu Pro
130	135	140
Gly Asp Ser Gly Gly Ala	Leu Phe Ala Gly Ser	Thr Ala Leu Gly Leu
145	150	155
Thr Ser Gly Gly Ser Gly	Asn Cys Arg Thr Gly	Gly Thr Thr Phe Phe
165	170	175
Gln Pro Val Thr Glu Ala	Leu Ser Ala Tyr Gly	Val Ser Ile Leu
180	185	190

<210> 629
 <211> 181
 <212> PRT

<213> Streptomyces griseus

<400> 629

Ile Ala Gly Gly Glu Ala Ile Thr Thr Gly Gly Ser Arg Cys Ser Leu
1 5 10 15
Gly Phe Asn Val Ser Val Asn Gly Val Ala His Ala Leu Thr Ala Gly
20 25 30
His Cys Thr Asn Ile Ser Ala Ser Trp Ser Ile Gly Thr Arg Thr Gly
35 40 45
Thr Ser Phe Pro Asn Asn Asp Tyr Gly Ile Ile Arg His Ser Asn Pro
50 55 60
Ala Ala Ala Asp Gly Arg Val Tyr Leu Tyr Asn Gly Ser Tyr Gln Asp
65 70 75 80
Ile Thr Thr Ala Gly Asn Ala Phe Val Gly Gln Ala Val Gln Arg Ser
85 90 95
Gly Ser Thr Thr Gly Leu Arg Ser Gly Ser Val Thr Gly Leu Asn Ala
100 105 110
Thr Val Asn Tyr Gly Ser Ser Gly Ile Val Tyr Gly Met Ile Gln Thr
115 120 125
Asn Val Cys Ala Gln Pro Gly Asp Ser Gly Gly Ser Leu Phe Ala Gly
130 135 140
Ser Thr Ala Leu Gly Leu Thr Ser Gly Gly Ser Gly Asn Cys Arg Thr
145 150 155 160
Gly Gly Thr Thr Phe Tyr Gln Pro Val Thr Glu Ala Leu Ser Ala Tyr
165 170 175
Gly Ala Thr Val Leu
180

<210> 630

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 630

Pro Arg Thr Met Phe Asp
1 5

<210> 631

<211> 10

<212> PRT

<213> Cellulomonas strain 69B4

<400> 631

Phe Asp Val Ile Gly Gly Asn Ala Tyr Thr
1 5 10

<210> 632

<211> 9

<212> PRT

<213> Cellulomonas strain 69B4

<400> 632

Thr Ala Asn Pro Thr Gly Thr Phe Ala
1 5

<210> 633

<211> 12

<212> PRT

<213> Cellulomonas strain 69B4

<400> 633

Phe Ala Gly Ser Ser Phe Pro Gly Asn Asp Tyr Ala
1 5 10

<210> 634

<211> 14

<212> PRT

<213> Cellulomonas strain 69B4

<400> 634

Phe Ala Gly Ser Ser Phe Pro Gly Asn Asp Tyr Ala Phe Val
1 5 10

<210> 635

<211> 10

<212> PRT

<213> Cellulomonas strain 69B4

<400> 635

Arg Thr Gly Ala Gly Val Asn Leu Leu Ala
1 5 10

<210> 636

<211> 9

<212> PRT

<213> Cellulomonas strain 69B4

<400> 636

Phe Phe Gln Pro Val Asn Pro Ile Leu
1 5

<210> 637

<211> 11

<212> PRT

<213> Cellulomonas strain 69B4

<400> 637

Phe Phe Gln Pro Val Asn Pro Ile Leu Gln Ala
1 5 10

<210> 638
 <211> 13
 <212> PRT
 <213> Cellulomonas strain 69B4

<400> 638

Phe Phe Gln Pro Val Asn Pro Ile Leu Gln Ala Tyr Gly
 1 5 10

<210> 639
 <211> 255
 <212> PRT
 <213> Streptogrisin C

<400> 639

Ala Asp Ile Arg Gly Gly Asp Ala Tyr Tyr Met Asn Gly Ser Gly Arg
 1 5 10 15
 Cys Ser Val Gly Phe Ser Val Thr Arg Gly Thr Gln Asn Gly Phe Ala
 20 25 30
 Thr Ala Gly His Cys Gly Arg Val Gly Thr Thr Thr Asn Gly Val Asn
 35 40 45
 Gln Gln Ala Gln Gly Thr Phe Gln Gly Ser Thr Phe Pro Gly Arg Asp
 50 55 60
 Ile Ala Trp Val Ala Thr Asn Ala Asn Trp Thr Pro Arg Pro Leu Val
 65 70 75 80
 Asn Gly Tyr Gly Arg Gly Asp Val Thr Val Ala Gly Ser Thr Ala Ser
 85 90 95
 Val Val Gly Ala Ser Val Cys Arg Ser Gly Ser Thr Thr Gly Trp His
 100 105 110
 Cys Gly Thr Ile Gln Gln Leu Asn Thr Ser Val Thr Tyr Pro Glu Gly
 115 120 125
 Thr Ile Ser Gly Val Thr Arg Thr Ser Val Cys Ala Glu Pro Gly Asp
 130 135 140
 Ser Gly Gly Ser Tyr Ile Ser Gly Ser Gln Ala Gln Gly Val Thr Ser
 145 150 155 160
 Gly Gly Ser Gly Asn Cys Ser Ser Gly Gly Thr Thr Tyr Phe Gln Pro
 165 170 175
 Ile Asn Pro Leu Leu Gln Ala Tyr Gly Leu Thr Leu Val Thr Ser Gly
 180 185 190
 Gly Gly Thr Pro Thr Asp Pro Pro Thr Thr Pro Pro Thr Asp Ser Pro
 195 200 205
 Gly Gly Thr Trp Ala Val Gly Thr Ala Tyr Ala Ala Gly Ala Thr Val
 210 215 220
 Thr Tyr Gly Gly Ala Thr Tyr Arg Cys Leu Gln Ala His Thr Ala Gln
 225 230 235 240
 Pro Gly Trp Thr Pro Ala Asp Val Pro Ala Leu Trp Gln Arg Val
 245 250 255

<210> 640
 <211> 185
 <212> PRT
 <213> Streptogrisin B

<400> 640

Ile Ser Gly Gly Asp Ala Ile Tyr Ser Ser Thr Gly Arg Cys Ser Leu
 1 5 10 15
 Gly Phe Asn Val Arg Ser Gly Ser Thr Tyr Tyr Phe Leu Thr Ala Gly

20 25 30
 His Cys Thr Asp Gly Ala Thr Thr Trp Trp Ala Asn Ser Ala Arg Thr
 35 40 45
 Thr Val Leu Gly Thr Thr Ser Gly Ser Ser Phe Pro Asn Asn Asp Tyr
 50 55 60
 Gly Ile Val Arg Tyr Thr Asn Thr Thr Ile Pro Lys Asp Gly Thr Val
 65 70 75 80
 Gly Gly Gln Asp Ile Thr Ser Ala Ala Asn Ala Thr Val Gly Met Ala
 85 90 95
 Val Thr Arg Arg Gly Ser Thr Thr Gly Thr His Ser Gly Ser Val Thr
 100 105 110
 Ala Leu Asn Ala Thr Val Asn Tyr Gly Gly Gly Asp Val Val Tyr Gly
 115 120 125
 Met Ile Arg Thr Asn Val Cys Ala Glu Pro Gly Asp Ser Gly Gly Pro
 130 135 140
 Leu Tyr Ser Gly Thr Arg Ala Ile Gly Leu Thr Ser Gly Gly Ser Gly
 145 150 155 160
 Asn Cys Ser Ser Gly Gly Thr Thr Phe Phe Gln Pro Val Thr Glu Ala
 165 170 175
 Leu Ser Ala Tyr Gly Val Ser Val Tyr
 180 185

<210> 641

<211> 181

<212> PRT

<213> Streptogrisin A

<400> 641

Ile Ala Gly Gly Glu Ala Ile Thr Thr Gly Gly Ser Arg Cys Ser Leu
 1 5 10 15
 Gly Phe Asn Val Ser Val Asn Gly Val Ala His Ala Leu Thr Ala Gly
 20 25 30
 His Cys Thr Asn Ile Ser Ala Ser Trp Ser Ile Gly Thr Arg Thr Gly
 35 40 45
 Thr Ser Phe Pro Asn Asn Asp Tyr Gly Ile Ile Arg His Ser Asn Pro
 50 55 60
 Ala Ala Ala Asp Gly Arg Val Tyr Leu Tyr Asn Gly Ser Tyr Gln Asp
 65 70 75 80
 Ile Thr Thr Ala Gly Asn Ala Phe Val Gly Gln Ala Val Gln Arg Ser
 85 90 95
 Gly Ser Thr Thr Gly Leu Arg Ser Gly Ser Val Thr Gly Leu Asn Ala
 100 105 110
 Thr Val Asn Tyr Gly Ser Ser Gly Ile Val Tyr Gly Met Ile Gln Thr
 115 120 125
 Asn Val Cys Ala Glu Pro Gly Asp Ser Gly Gly Ser Leu Phe Ala Gly
 130 135 140
 Ser Thr Ala Leu Gly Leu Thr Ser Gly Gly Ser Gly Asn Cys Arg Thr
 145 150 155 160
 Gly Gly Thr Thr Phe Tyr Gln Pro Val Thr Glu Ala Leu Ser Ala Tyr
 165 170 175
 Gly Ala Thr Val Leu

180

<210> 642
<211> 188
<212> PRT
<213> Streptogrisin D

<400> 642

Ile	Ala	Gly	Gly	Asp	Ala	Ile	Trp	Gly	Ser	Gly	Ser	Arg	Cys	Ser	Leu
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Gly	Phe	Asn	Val	Val	Lys	Gly	Gly	Glu	Pro	Tyr	Phe	Leu	Thr	Ala	Gly
		20						25				30			
His	Cys	Thr	Glu	Ser	Val	Thr	Ser	Trp	Ser	Asp	Thr	Gln	Gly	Gly	Ser
	35						40					45			
Glu	Ile	Gly	Ala	Asn	Glu	Gly	Ser	Ser	Phe	Pro	Glu	Asn	Asp	Tyr	Gly
	50					55				60					
Leu	Val	Lys	Tyr	Thr	Ser	Asp	Thr	Ala	His	Pro	Ser	Glu	Val	Asn	Leu
65					70				75					80	
Tyr	Asp	Gly	Ser	Thr	Gln	Ala	Ile	Thr	Gln	Ala	Gly	Asp	Ala	Thr	Val
				85				90						95	
Gly	Gln	Ala	Val	Thr	Arg	Ser	Gly	Ser	Thr	Thr	Gln	Val	His	Asp	Gly

			100					105					110		
Glu	Val	Thr	Ala	Leu	Asp	Ala	Thr	Val	Asn	Tyr	Gly	Asn	Gly	Asp	Ile
		115					120					125			
Val	Asn	Gly	Leu	Ile	Gln	Thr	Thr	Val	Cys	Ala	Glu	Pro	Gly	Asp	Ser
	130					135					140				
Gly	Gly	Ala	Leu	Phe	Ala	Gly	Asp	Thr	Ala	Leu	Gly	Leu	Thr	Ser	Gly
145					150					155				160	
Gly	Ser	Gly	Asp	Cys	Ser	Ser	Gly	Gly	Thr	Thr	Phe	Phe	Gln	Pro	Val
			165					170						175	
Pro	Glu	Ala	Leu	Ala	Ala	Tyr	Gly	Ala	Glu	Ile	Gly				
			180					185							

<210> 643
<211> 198
<212> PRT
<213> Artificial Sequence

<220>
<223> consensus sequence

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<222> (9)..(10)
<223> Xaa can be any naturally occurring amino acid

<220>
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<222> (12)..(12)
<223> Xaa can be any naturally occurring amino acid

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<223> Xaa can be any naturally occurring amino acid

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Leu	Gly	Phe	Asn	Val	Xaa	Xaa	Gly	Xaa	Xaa	Xaa	Tyr	Phe	Leu	Thr	Ala
			20					25					30		
Gly	His	Cys	Thr	Xaa	Xaa	Gly	Thr	Thr	Trp	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
		35					40					45			
Xaa	Xaa	Xaa	Ile	Gly	Thr	Xaa	Xaa	Gly	Ser	Ser	Phe	Pro	Xaa	Asn	Asp
	50					55					60				
Tyr	Gly	Ile	Val	Arg	Tyr	Thr	Ala	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Val
65				70					75						80
Asn	Xaa	Tyr	Xaa	Gly	Xaa	Xaa	Gln	Xaa	Ile	Thr	Xaa	Ala	Gly	Xaa	Ala
			85					90					95		
Xaa	Val	Gly	Xaa	Ala	Val	Xaa	Arg	Ser	Gly	Ser	Thr	Thr	Gly	Xaa	His
		100					105						110		
Xaa	Gly	Ser	Val	Thr	Ala	Leu	Asn	Ala	Thr	Val	Asn	Tyr	Gly	Xaa	Gly
	115						120						125		
Xaa	Ile	Val	Xaa	Gly	Leu	Ile	Arg	Thr	Thr	Val	Cys	Ala	Glu	Pro	Gly
	130					135					140				
Asp	Ser	Gly	Gly	Ser	Leu	Phe	Ala	Gly	Ser	Xaa	Ala	Leu	Gly	Leu	Thr
145					150					155					160
Ser	Gly	Gly	Ser	Gly	Asn	Cys	Ser	Ser	Gly	Gly	Thr	Thr	Phe	Phe	Gln
			165						170					175	
Pro	Val	Xaa	Glu	Ala	Leu	Ser	Ala	Tyr	Gly	Leu	Thr	Val	Ile	Xaa	Xaa
		180						185					190		
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa										
		195													

<210> 644
 <211> 513
 <212> PRT
 <213> Thermus aquaticus

<400> 644

Met	Arg	Lys	Thr	Tyr	Trp	Leu	Met	Ala	Leu	Phe	Ala	Val	Leu	Val	Leu
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Gly	Gly	Cys	Gln	Met	Ala	Ser	Arg	Ser	Asp	Pro	Thr	Pro	Thr	Leu	Ala
		20						25					30		
Glu	Ala	Phe	Trp	Pro	Lys	Glu	Ala	Pro	Val	Tyr	Gly	Leu	Asp	Asp	Pro
	35						40					45			
Glu	Ala	Ile	Pro	Gly	Arg	Tyr	Ile	Val	Val	Phe	Lys	Lys	Gly	Lys	Gly
	50					55				60					
Gln	Ser	Leu	Leu	Gln	Gly	Gly	Ile	Thr	Thr	Leu	Gln	Ala	Arg	Leu	Ala
65				70					75						80
Pro	Gln	Gly	Val	Val	Val	Thr	Gln	Ala	Tyr	Thr	Gly	Ala	Leu	Gln	Gly
			85					90					95		
Phe	Ala	Ala	Glu	Met	Ala	Pro	Gln	Ala	Leu	Glu	Ala	Phe	Arg	Gln	Ser
		100					105						110		
Pro	Asp	Val	Glu	Phe	Ile	Glu	Ala	Asp	Lys	Val	Val	Arg	Ala	Trp	Ala
	115						120					125			
Thr	Gln	Ser	Pro	Ala	Pro	Trp	Gly	Leu	Asp	Arg	Ile	Asp	Gln	Arg	Asp

130		135		140	
Leu	Pro	Leu	Ser	Asn	Ser
145		150		155	
Asn	Val	Tyr	Val	Ile	Asp
		165		170	
Gly	Gly	Arg	Ala	Arg	Val
		180		185	
Asp	Cys	Asn	Gly	His	Gly
		195		200	
Thr	Tyr	Gly	Val	Ala	Lys
		210		215	
Asp	Cys	Asn	Gly	Ser	Gly
225		230		235	
Trp	Val	Thr	Arg	Asn	His
		245		250	
Gly	Gly	Gly	Val	Ser	Thr
		260		265	
Ala	Ala	Gly	Val	Val	Tyr
		275		280	
Ala	Cys	Asn	Tyr	Ser	Pro
		290		295	
Ala	Thr	Thr	Ser	Ser	Asp
305		310		315	
Cys	Val	Asp	Leu	Phe	Ala
		325		330	
Thr	Ser	Asp	Thr	Ala	Thr
		340		345	
Pro	His	Val	Ala	Gly	Val
		355		360	
Ala	Thr	Pro	Ala	Ser	Val
		370		375	
Gly	Arg	Leu	Ser	Gly	Ile
385		390		395	
Ser	Leu	Leu	Ser	Ser	Gly
		405		410	
Ser	Tyr	Tyr	Thr	Gly	Ser
		420		425	
Pro	Asn	Gly	Thr	Tyr	Tyr
		435		440	
Leu	Arg	Gly	Pro	Ala	Gly
		450		455	
Asp	Gly	Ser	Arg	Trp	Leu
465		470		475	
Glu	Glu	Ser	Leu	Ser	Tyr
		485		490	
Ile	Tyr	Ala	Tyr	Ser	Gly
		500		505	
Pro					

<210> 645
 <211> 495
 <212> PRT
 <213> Cellulomonas strain 69B4

 <400> 645

Met	Thr	Pro	Arg	Thr	Val	Thr	Arg	Ala	Leu	Ala	Val	Ala	Thr	Ala	Ala	
1				5					10					15		
Ala	Thr	Leu	Leu	Ala	Gly	Gly	Met	Ala	Ala	Gln	Ala	Asn	Glu	Pro	Ala	
		20					25					30				
Pro	Pro	Gly	Ser	Ala	Ser	Ala	Pro	Pro	Arg	Leu	Ala	Glu	Lys	Leu	Asp	
	35						40					45				
Pro	Asp	Leu	Leu	Glu	Ala	Met	Glu	Arg	Asp	Leu	Gly	Leu	Asp	Ala	Glu	
	50					55					60					
Glu	Ala	Ala	Ala	Thr	Leu	Ala	Phe	Gln	His	Asp	Ala	Ala	Glu	Thr	Gly	
65				70					75						80	
Glu	Ala	Leu	Ala	Glu	Glu	Leu	Asp	Glu	Asp	Phe	Ala	Gly	Thr	Trp	Val	
			85					90						95		
Glu	Asp	Asp	Val	Leu	Tyr	Val	Ala	Thr	Thr	Asp	Glu	Asp	Ala	Val	Glu	
			100					105					110			
Glu	Val	Glu	Gly	Glu	Gly	Ala	Thr	Ala	Val	Thr	Val	Glu	His	Ser	Leu	
	115						120					125				
Ala	Asp	Leu	Glu	Ala	Trp	Lys	Thr	Val	Leu	Asp	Ala	Ala	Leu	Glu	Gly	
	130					135					140					
His	Asp	Asp	Val	Pro	Thr	Trp	Tyr	Val	Asp	Val	Pro	Thr	Asn	Ser	Val	
145				150					155						160	
Val	Val	Ala	Val	Lys	Ala	Gly	Ala	Gln	Asp	Val	Ala	Ala	Gly	Leu	Val	
			165					170						175		
Glu	Gly	Ala	Asp	Val	Pro	Ser	Asp	Ala	Val	Thr	Phe	Val	Glu	Thr	Asp	
		180						185					190			
Glu	Thr	Pro	Arg	Thr	Met	Phe	Asp	Val	Ile	Gly	Gly	Asn	Ala	Tyr	Thr	
	195						200					205				
Ile	Gly	Gly	Arg	Ser	Arg	Cys	Ser	Ile	Gly	Phe	Ala	Val	Asn	Gly	Gly	
	210					215					220					
Phe	Ile	Thr	Ala	Gly	His	Cys	Gly	Arg	Thr	Gly	Ala	Thr	Thr	Ala	Asn	
225				230					235						240	
Pro	Thr	Gly	Thr	Phe	Ala	Gly	Ser	Ser	Phe	Pro	Gly	Asn	Asp	Tyr	Ala	
			245						250					255		
Phe	Val	Arg	Thr	Gly	Ala	Gly	Val	Asn	Leu	Leu	Ala	Gln	Val	Asn	Asn	
		260						265					270			
Tyr	Ser	Gly	Gly	Arg	Val	Gln	Val	Ala	Gly	His	Thr	Ala	Ala	Pro	Val	
	275						280					285				
Gly	Ser	Ala	Val	Cys	Arg	Ser	Gly	Ser	Thr	Thr	Gly	Trp	His	Cys	Gly	
	290					295					300					
Thr	Ile	Thr	Ala	Leu	Asn	Ser	Ser	Val	Thr	Tyr	Pro	Glu	Gly	Thr	Val	
305				310					315						320	
Arg	Gly	Leu	Ile	Arg	Thr	Thr	Val	Cys	Ala	Glu	Pro	Gly	Asp	Ser	Gly	
			325					330						335		
Gly	Ser	Leu	Leu	Ala	Gly	Asn	Gln	Ala	Gln	Gly	Val	Thr	Ser	Gly	Gly	
		340						345					350			
Ser	Gly	Asn	Cys	Arg	Thr	Gly	Gly	Thr	Thr	Phe	Phe	Gln	Pro	Val	Asn	
	355						360					365				
Pro	Ile	Leu	Gln	Ala	Tyr	Gly	Leu	Arg	Met	Ile	Thr	Thr	Asp	Ser	Gly	
	370					375					380					
Ser	Ser	Pro	Ala	Pro	Ala	Pro	Thr	Ser	Cys	Thr	Gly	Tyr	Ala	Arg	Thr	
385				390					395						400	
Phe	Thr	Gly	Thr	Leu	Ala	Ala	Gly	Arg	Ala	Ala	Ala	Gln	Pro	Asn	Gly	
			405					410						415		
Ser	Tyr	Val	Gln	Val	Asn	Arg	Ser	Gly	Thr	His	Ser	Val	Cys	Leu	Asn	
	420							425					430			
Gly	Pro	Ser	Gly	Ala	Asp	Phe	Asp	Leu	Tyr	Val	Gln	Arg	Trp	Asn	Gly	
	435						440					445				
Ser	Ser	Trp	Val	Thr	Val	Ala	Gln	Ser	Thr	Ser	Pro	Gly	Ser	Asn	Glu	

450	455	460
Thr Ile Thr Tyr Arg Gly Asn Ala Gly Tyr Tyr Arg Tyr Val Val Asn		
465	470	475
Ala Ala Ser Gly Ser Gly Ala Tyr Thr Met Gly Leu Thr Leu Pro		480
	485	490
		495

<210> 646
 <211> 510
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> consensus sequence

<220>
 <221> VARIANT
 <222> (3)..(509)
 <223> Xaa can be any naturally occurring amino acid

<400> 646

Met Ala Xaa Xaa Ala Xaa Xaa Leu Leu Ala Gly Xaa Xaa Xaa Ala Xaa		
1	5	10
Xaa Xaa Asp Pro Xaa Pro Xaa Xaa Ala Xaa Ala Xaa Xaa Pro Lys Xaa		15
	20	25
Ala Xaa Xaa Xaa Xaa Xaa Asp Xaa Xaa Glu Ala Ile Xaa Xaa Xaa Xaa		30
	35	40
Xaa Leu Xaa Xaa Xaa Xaa Xaa Ala Xaa Xaa Xaa Xaa Gln Xaa Xaa		45
	50	55
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Leu Ala Xaa Xaa Xaa Xaa Xaa Xaa Xaa		60
65	70	75
Xaa Xaa Phe Xaa Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa		80
	85	90
Xaa Xaa Xaa Glu Xaa Xaa Xaa Xaa Xaa Xaa Asp Xaa Glu Xaa Xaa Xaa		95
	100	105
Ala Xaa Xaa Val Xaa Xaa Ala Xaa Ala Xaa Xaa Xaa Xaa Xaa Xaa Xaa		110
	115	120
Xaa Leu Asp Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Tyr		125
	130	135
Xaa Xaa Xaa Xaa Thr Xaa Xaa Xaa Xaa Xaa Xaa Val Xaa Xaa Ile Xaa Xaa		140
145	150	155
Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ala Xaa Val Xaa		160
	165	170
Xaa Asp Ala Leu Xaa Xaa Xaa Xaa Xaa Asp Xaa Xaa Xaa Xaa Xaa Xaa		175
	180	185
Xaa Met Xaa Xaa Xaa Ile Gly Gly Xaa Xaa Tyr Xaa Ile Ala Xaa Xaa		190
	195	200
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Ala		205
	210	215
Xaa Xaa Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Arg Xaa Xaa Xaa		220
225	230	235
Xaa Xaa Ala Xaa Xaa Xaa Xaa Ser Xaa Ala Gly Xaa Xaa Xaa Xaa Ala		240
	245	250
Xaa Asp Xaa Ala Xaa Xaa Xaa Ser Xaa Ala Ala Xaa Xaa Xaa Xaa Xaa		255
	260	265
Xaa Xaa Xaa Xaa Asn Xaa Xaa Ala Asn Xaa Xaa Asn Tyr Ser Xaa Ala		270
	275	280
		285

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Arg Val Xaa Xaa Ala Xaa Xaa Xaa Ala Ala Xaa Xaa Xaa Ser Xaa Xaa
 290                295                300
Xaa Xaa Ser Xaa Ser Xaa Xaa Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa
305                310                315                320
Xaa Ala Xaa Xaa Xaa Ser Xaa Xaa Tyr Xaa Xaa Xaa Thr Xaa Xaa Xaa
      325                330                335
Xaa Ile Xaa Xaa Thr Xaa Xaa Ala Xaa Pro Xaa Xaa Ala Gly Xaa Ala
      340                345                350
Xaa Leu Xaa Xaa Xaa Gln Xaa Xaa Xaa Xaa Thr Xaa Ala Xaa Xaa Ala
      355                360                365
Xaa Xaa Xaa Xaa Xaa Gly Xaa Thr Xaa Xaa Xaa Xaa Xaa Xaa Xaa
      370                375                380
Xaa Xaa Ala Xaa Xaa Xaa Xaa Leu Xaa Ser Xaa Xaa Ser Xaa Gly Ser
385                390                395                400
Xaa Xaa Xaa Xaa Xaa Xaa Thr Ser Cys Ser Xaa Tyr Xaa Xaa Ser Xaa
      405                410                415
Ser Gly Xaa Xaa Xaa Xaa Gly Xaa Xaa Xaa Xaa Gln Pro Asn Gly Ser
      420                425                430
Tyr Xaa Xaa Xaa Xaa Xaa Ala Gly Thr His Xaa Xaa Xaa Leu Xaa Gly
      435                440                445
Pro Ala Gly Xaa Asp Phe Asp Leu Tyr Leu Xaa Arg Trp Xaa Gly Ser
      450                455                460
Xaa Trp Leu Thr Val Ala Xaa Ser Thr Xaa Pro Xaa Ser Xaa Glu Ser
465                470                475                480
Ile Ser Tyr Xaa Gly Xaa Ala Gly Tyr Tyr Xaa Trp Xaa Ile Xaa Ala
      485                490                495
Xaa Ser Gly Ser Gly Xaa Tyr Xaa Xaa Xaa Leu Xaa Xaa Pro
      500                505                510

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<210> 647

<211> 190

<212> PRT

<213> Artificial Sequence

<220>

<223> consensus sequence

<220>

<221> VARIANT

<222> (6)..(188)

<223> Xaa can be any naturally occurring amino acid

<400> 647

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Asp Val Ile Gly Gly Xaa Xaa Tyr Xaa Ile Xaa Xaa Xaa Xaa Arg Xaa
 1          5          10          15
Xaa Xaa Xaa Xaa Cys Ser Ile Gly Phe Ala Val Xaa Gly Gly Phe Val
      20          25          30
Thr Ala Gly His Cys Gly Arg Xaa Gly Ala Xaa Xaa Xaa Xaa Xaa
      35          40          45
Thr Ser Xaa Pro Xaa Gly Thr Phe Xaa Gly Ser Ser Phe Pro Gly Asn
      50          55          60
Asp Tyr Ala Trp Val Gln Val Ala Ser Gly Asn Thr Pro Val Gly Ala
65          70          75          80
Val Asn Asn Tyr Ser Gly Gly Thr Val Xaa Val Ala Gly Ser Thr Xaa
      85          90          95
Ala Ala Val Gly Ala Ser Val Cys Arg Ser Gly Ser Thr Thr Gly Trp

```


Gly	Thr	Val	Thr	Gly	Leu	Thr	Arg	Thr	Thr	Ala	Cys	Ala	Glu	Gly	Gly
305					310					315					320
Asp	Ser	Gly	Gly	Pro	Trp	Leu	Thr	Gly	Ser	Gln	Ala	Gln	Gly	Val	Thr
				325					330					335	
Ser	Gly	Gly	Thr	Gly	Asp	Cys	Arg	Ser	Gly	Gly	Ile	Thr	Phe	Phe	Gln
			340					345					350		
Pro	Ile	Asn	Pro	Leu	Leu	Ser	Tyr	Phe	Gly	Leu	Gln	Leu	Val	Thr	Gly
		355					360					365			

<210> 649

<211> 382

<212> PRT

<213> Streptomyces spp.

<400> 649

Met	Arg	His	Thr	Gly	Arg	Asn	Ala	Ile	Gly	Ala	Ala	Ile	Ala	Ala	Ser
1				5					10				15		
Ala	Leu	Ala	Phe	Ala	Leu	Val	Pro	Ser	Gln	Ala	Ala	Ala	Asn	Asp	Thr
			20					25					30		
Leu	Thr	Glu	Arg	Ala	Glu	Ala	Ala	Val	Ala	Asp	Leu	Pro	Ala	Gly	Val
		35				40						45			
Leu	Asp	Ala	Met	Glu	Arg	Asp	Leu	Gly	Leu	Ser	Glu	Gln	Glu	Ala	Gly
	50					55					60				
Leu	Lys	Leu	Val	Ala	Glu	His	Asp	Ala	Ala	Leu	Leu	Gly	Glu	Thr	Leu
65					70					75					80
Ser	Ala	Asp	Leu	Asp	Ala	Phe	Ala	Gly	Ser	Trp	Leu	Ala	Glu	Gly	Thr
				85					90					95	
Glu	Leu	Val	Val	Ala	Thr	Thr	Ser	Glu	Ala	Glu	Ala	Ala	Glu	Ile	Thr
			100					105					110		
Glu	Ala	Gly	Ala	Thr	Ala	Glu	Val	Val	Asp	His	Thr	Leu	Ala	Glu	Leu
		115					120					125			
Asp	Ser	Val	Lys	Asp	Ala	Leu	Asp	Thr	Ala	Ala	Glu	Ser	Tyr	Asp	Thr
	130					135					140				
Thr	Asp	Ala	Pro	Val	Trp	Tyr	Val	Asp	Val	Thr	Thr	Asn	Gly	Val	Val
145					150					155					160
Leu	Leu	Thr	Ser	Asp	Val	Thr	Glu	Ala	Glu	Gly	Phe	Val	Glu	Ala	Ala
				165					170					175	
Gly	Val	Asn	Ala	Ala	Ala	Val	Asp	Ile	Gln	Thr	Ser	Asp	Glu	Gln	Pro
		180					185						190		
Gln	Ala	Phe	Tyr	Asp	Leu	Val	Gly	Gly	Asp	Ala	Tyr	Tyr	Met	Gly	Gly
	195					200						205			
Gly	Arg	Cys	Ser	Val	Gly	Phe	Ser	Val	Thr	Gln	Gly	Ser	Thr	Pro	Gly
	210					215					220				
Phe	Ala	Thr	Ala	Gly	His	Cys	Gly	Thr	Val	Gly	Thr	Ser	Thr	Thr	Gly
225					230					235					240
Tyr	Asn	Gln	Ala	Ala	Gln	Gly	Thr	Phe	Glu	Glu	Ser	Ser	Phe	Pro	Gly
				245					250					255	
Asp	Asp	Met	Ala	Trp	Val	Ser	Val	Asn	Ser	Asp	Trp	Asn	Thr	Thr	Pro
		260						265					270		
Thr	Val	Asn	Glu	Gly	Glu	Val	Thr	Val	Ser	Gly	Ser	Thr	Glu	Ala	Ala
		275					280					285			
Val	Gly	Ala	Ser	Ile	Cys	Arg	Ser	Gly	Ser	Thr	Thr	Gly	Trp	His	Cys
	290					295					300				
Gly	Thr	Ile	Gln	Gln	His	Asn	Thr	Ser	Val	Thr	Tyr	Pro	Glu	Gly	Thr
305					310					315					320
Ile	Thr	Gly	Val	Thr	Arg	Thr	Ser	Val	Cys	Ala	Glu	Pro	Gly	Asp	Ser

				325					330				335				
Gly	Gly	Ser	Tyr	Ile	Ser	Gly	Ser	Gln	Ala	Gln	Gly	Val	Thr	Ser	Gly		
			340					345					350				
Gly	Ser	Gly	Asn	Cys	Thr	Ser	Gly	Gly	Thr	Thr	Tyr	His	Gln	Pro	Ile		
		355					360					365					
Asn	Pro	Leu	Leu	Ser	Ala	Tyr	Gly	Leu	Asp	Leu	Val	Thr	Gly				
	370					375					380						

<210> 650
 <211> 388
 <212> PRT
 <213> Streptomyces spp.

<400> 650

Met	Arg	Leu	Lys	Gly	Arg	Thr	Val	Ala	Ile	Gly	Ser	Ala	Leu	Ala	Ala		
1			5					10					15				
Ser	Ala	Leu	Ala	Leu	Ser	Leu	Val	Pro	Ala	Asn	Ala	Ser	Ser	Glu	Leu		
		20						25					30				
Pro	Ser	Ala	Glu	Thr	Ala	Lys	Ala	Asp	Ala	Leu	Val	Glu	Gln	Leu	Pro		
		35				40						45					
Ala	Gly	Met	Val	Asp	Ala	Met	Glu	Arg	Asp	Leu	Gly	Val	Pro	Ala	Ala		
	50				55						60						
Glu	Val	Gly	Asn	Gln	Leu	Val	Ala	Glu	His	Glu	Ala	Ala	Val	Leu	Glu		
65				70				75						80			
Glu	Ser	Leu	Ser	Glu	Asp	Leu	Ser	Gly	Tyr	Ala	Gly	Ser	Trp	Ile	Val		
			85					90					95				
Glu	Gly	Thr	Ser	Glu	His	Val	Val	Ala	Thr	Thr	Asp	Arg	Ala	Glu	Ala		
		100						105					110				
Ala	Glu	Ile	Thr	Ala	Ala	Gly	Ala	Thr	Ala	Thr	Val	Val	Glu	His	Ser		
	115					120						125					
Leu	Ala	Glu	Leu	Glu	Ala	Val	Lys	Asp	Ile	Leu	Asp	Glu	Ala	Ala	Thr		
	130					135					140						
Ala	Asn	Pro	Glu	Asp	Ala	Ala	Pro	Val	Trp	Tyr	Val	Asp	Val	Thr	Thr		
145				150					155					160			
Asn	Glu	Val	Val	Val	Leu	Ala	Ser	Asp	Val	Pro	Ala	Ala	Glu	Ala	Phe		
			165					170					175				
Val	Ala	Ala	Ser	Gly	Ala	Asp	Ala	Ser	Thr	Val	Arg	Val	Glu	Arg	Ser		
		180				185						190					
Asp	Glu	Ser	Pro	Gln	Pro	Phe	Tyr	Asp	Leu	Val	Gly	Gly	Asp	Ala	Tyr		
	195					200						205					
Tyr	Ile	Gly	Asn	Gly	Arg	Cys	Ser	Ile	Gly	Phe	Ser	Val	Arg	Gln	Gly		
	210				215						220						
Ser	Thr	Pro	Gly	Phe	Val	Thr	Ala	Gly	His	Cys	Gly	Ser	Val	Gly	Asn		
225				230					235					240			
Ala	Thr	Thr	Gly	Phe	Asn	Arg	Val	Ser	Gln	Gly	Thr	Phe	Arg	Gly	Ser		
			245					250						255			
Trp	Phe	Pro	Gly	Arg	Asp	Met	Ala	Trp	Val	Ala	Val	Asn	Ser	Asn	Trp		
		260						265					270				
Thr	Pro	Thr	Ser	Leu	Val	Arg	Asn	Ser	Gly	Ser	Gly	Val	Arg	Val	Thr		
	275					280						285					
Gly	Ser	Thr	Gln	Ala	Thr	Val	Gly	Ser	Ser	Ile	Cys	Arg	Ser	Gly	Ser		
	290				295						300						
Thr	Thr	Gly	Trp	Arg	Cys	Gly	Thr	Ile	Gln	Gln	His	Asn	Thr	Ser	Val		
305				310					315					320			
Thr	Tyr	Pro	Gln	Gly	Thr	Ile	Thr	Gly	Val	Thr	Arg	Thr	Ser	Ala	Cys		
			325					330					335				

Ala Gln Pro Gly Asp Ser Gly Gly Ser Phe Ile Ser Gly Thr Gln Ala
340 345 350
Gln Gly Val Thr Ser Gly Gly Ser Gly Asn Cys Ser Ile Gly Gly Thr
355 360 365
Thr Phe His Gln Pro Val Asn Pro Ile Leu Ser Gln Tyr Gly Leu Thr
370 375 380
Leu Val Arg Ser
385

<210> 651

<211> 458

<212> PRT

<213> Streptomyces lividans

<400> 651

Met Val Gly Arg His Ala Ala Arg Ser Arg Arg Ala Ala Leu Thr Ala
1 5 10 15
Leu Gly Ala Leu Val Leu Thr Ala Leu Pro Ser Ala Ala Ser Ala Ala
20 25 30
Pro Pro Pro Val Pro Gly Pro Arg Pro Ala Val Ala Arg Thr Pro Asp
35 40 45
Ala Ala Thr Ala Pro Ala Arg Met Leu Ser Ala Met Glu Arg Asp Leu
50 55 60
Arg Leu Ala Pro Gly Gln Ala Ala Ala Arg Pro Val Asn Glu Ala Glu
65 70 75 80
Ala Gly Thr Arg Ala Gly Met Leu Arg Asn Thr Leu Gly Asp Arg Phe
85 90 95
Ala Gly Ala Trp Val Ser Gly Ala Thr Ser Ala Glu Leu Thr Val Ala
100 105 110
Thr Thr Asp Ala Ala Asp Thr Ala Ala Ile Glu Ala Gln Gly Ala Lys
115 120 125
Ala Ala Val Val Gly Arg Asn Leu Ala Glu Leu Arg Ala Val Lys Glu
130 135 140
Lys Leu Asp Ala Ala Ala Val Arg Thr Arg Thr Arg Gln Thr Pro Val
145 150 155 160
Trp Tyr Val Asp Val Lys Thr Asn Arg Val Thr Val Gln Ala Thr Gly
165 170 175
Ala Ser Ala Ala Ala Ala Phe Val Glu Ala Ala Gly Val Pro Ala Ala
180 185 190
Asp Val Gly Val Arg Val Ser Pro Asp Gln Pro Arg Val Leu Glu Asp
195 200 205
Leu Val Gly Gly Asp Ala Tyr Tyr Ile Asp Asp Gln Ala Arg Cys Ser
210 215 220
Ile Gly Phe Ser Val Thr Lys Asp Asp Gln Glu Gly Phe Ala Thr Ala
225 230 235 240
Gly His Cys Gly Asp Pro Gly Ala Thr Thr Gly Tyr Asn Glu Ala
245 250 255
Asp Gln Gly Thr Phe Gln Ala Ser Thr Phe Pro Gly Lys Asp Met Ala
260 265 270
Trp Val Gly Val Asn Ser Asp Trp Thr Ala Thr Pro Asp Val Lys Ala
275 280 285
Glu Gly Gly Glu Lys Ile Gln Leu Ala Gly Ser Val Glu Ala Leu Val
290 295 300
Gly Ala Ser Val Cys Arg Ser Gly Ser Thr Thr Gly Trp His Cys Gly
305 310 315 320
Thr Ile Gln Gln His Asp Thr Ser Val Thr Tyr Pro Glu Gly Thr Val

Asp	Gln	Gly	Thr	Phe	Gln	Ala	Ser	Thr	Phe	Pro	Gly	Lys	Asp	Met	Ala	
			260					265					270			
Trp	Val	Gly	Val	Asn	Ser	Asp	Trp	Thr	Ala	Thr	Pro	Asp	Val	Lys	Ala	
		275					280					285				
Glu	Gly	Gly	Glu	Lys	Ile	Gln	Leu	Ala	Gly	Ser	Val	Glu	Ala	Leu	Val	
	290					295					300					
Gly	Ala	Ser	Val	Cys	Arg	Ser	Gly	Ser	Thr	Thr	Gly	Trp	His	Cys	Gly	
305					310					315					320	
Thr	Ile	Gln	Gln	His	Asp	Thr	Ser	Val	Thr	Tyr	Pro	Glu	Gly	Thr	Val	
				325					330					335		
Asp	Gly	Leu	Thr	Glu	Thr	Thr	Val	Cys	Ala	Glu	Pro	Gly	Asp	Ser	Gly	
		340						345				350				
Gly	Pro	Phe	Val	Ser	Gly	Val	Gln	Ala	Gln	Gly	Thr	Thr	Ser	Gly	Gly	
		355					360					365				
Ser	Gly	Asp	Cys	Thr	Asn	Gly	Gly	Thr	Thr	Phe	Tyr	Gln	Pro	Val	Asn	
	370					375				380						
Pro	Leu	Leu	Ser	Asp	Phe	Gly	Leu	Thr	Leu	Lys	Thr	Thr	Ser	Ala	Ala	
385					390					395					400	
Thr	Gln	Thr	Pro	Ala	Pro	Gln	Asp	Asn	Ala	Ala	Ala	Asp	Ala	Trp	Thr	
				405					410					415		
Ala	Gly	Arg	Val	Tyr	Glu	Val	Gly	Thr	Thr	Val	Ser	Tyr	Asp	Gly	Val	
		420						425					430			
Arg	Tyr	Arg	Cys	Leu	Gln	Ser	His	Gln	Ala	Gln	Gly	Val	Gly	Ser	Pro	
	435					440						445				
Ala	Ser	Val	Pro	Ala	Leu	Trp	Gln	Arg	Val							
	450					455										

<210> 653

<211> 456

<212> PRT

<213> Streptomyces avermitilis MA-4680

<400> 653

Met	Val	His	Arg	His	Val	Gly	Ala	Gly	Cys	Ala	Gly	Leu	Ser	Val	Leu	
1				5					10					15		
Ala	Thr	Leu	Val	Leu	Thr	Gly	Leu	Pro	Ala	Ala	Ala	Ala	Ile	Glu	Pro	
		20						25					30			
Pro	Gly	Pro	Ala	Pro	Ala	Pro	Ser	Ala	Val	Gln	Pro	Leu	Gly	Ala	Gly	
		35				40						45				
Asn	Pro	Ser	Thr	Ala	Val	Leu	Gly	Ala	Leu	Gln	Arg	Asp	Leu	His	Leu	
	50					55				60						
Thr	Asp	Thr	Gln	Ala	Lys	Thr	Arg	Leu	Val	Asn	Glu	Met	Glu	Ala	Gly	
65				70						75				80		
Thr	Arg	Ala	Gly	Arg	Leu	Gln	Asn	Ala	Leu	Gly	Lys	His	Phe	Ala	Gly	
			85					90					95			
Ala	Trp	Val	His	Gly	Ala	Ala	Ser	Ala	Asp	Leu	Thr	Val	Ala	Thr	Thr	
		100						105					110			
His	Ala	Thr	Asp	Ile	Pro	Ala	Ile	Thr	Ala	Gly	Gly	Ala	Thr	Ala	Val	
		115				120						125				
Val	Val	Lys	Thr	Gly	Leu	Asp	Leu	Lys	Gly	Ala	Lys	Lys	Lys	Lys	Leu	
	130					135				140						
Asp	Ser	Ala	Val	Ala	His	Gly	Gly	Thr	Ala	Val	Asn	Thr	Pro	Val	Arg	
145				150						155					160	
Tyr	Val	Asp	Val	Arg	Thr	Asn	Arg	Val	Thr	Leu	Gln	Ala	Arg	Ser	Arg	
			165					170					175			
Ala	Ala	Ala	Asp	Ala	Leu	Ile	Ala	Ala	Ala	Gly	Val	Asp	Ser	Gly	Leu	

Thr Thr Asp Ala Gly Asp Val Ala Ala Val Glu Ala Arg Gly Ala Glu
 115 120 125
 Ala Lys Val Val Arg His Ser Leu Ala Asp Leu Asp Ala Ala Lys Ala
 130 135 140
 Arg Leu Asp Thr Ala Ala Gly Leu Asn Thr Ala Asp Ala Pro Val
 145 150 155 160
 Trp Tyr Val Asp Thr Arg Thr Asn Thr Val Val Glu Ala Ile Arg
 165 170 175
 Pro Ala Ala Ala Arg Ser Leu Leu Thr Ala Ala Gly Val Asp Gly Ser
 180 185 190
 Leu Ala His Val Lys Asn Arg Thr Glu Arg Pro Arg Thr Phe Tyr Asp
 195 200 205
 Leu Arg Gly Gly Glu Ala Tyr Tyr Ile Asn Asn Ser Ser Arg Cys Ser
 210 215 220
 Ile Gly Phe Pro Ile Thr Lys Gly Thr Gln Gln Gly Phe Ala Thr Ala
 225 230 235 240
 Gly His Cys Asp Arg Ala Gly Ser Ser Thr Thr Gly Ala Asn Arg Val
 245 250 255
 Ala Gln Gly Thr Phe Gln Gly Ser Ile Phe Pro Gly Arg Asp Met Ala
 260 265 270
 Trp Val Ala Thr Asn Ser Ser Trp Thr Ala Thr Pro Tyr Val Leu Gly
 275 280 285
 Ala Gly Gly Gln Asn Val Gln Val Thr Gly Ser Thr Ala Ser Pro Val
 290 295 300
 Gly Ala Ser Val Cys Arg Ser Gly Ser Thr Thr Gly Trp His Cys Gly
 305 310 315 320
 Thr Val Thr Gln Leu Asn Thr Ser Val Thr Tyr Gln Glu Gly Thr Ile
 325 330 335
 Ser Pro Val Thr Arg Thr Thr Val Cys Ala Glu Pro Gly Asp Ser Gly
 340 345 350
 Gly Ser Phe Ile Ser Gly Ser Gln Ala Gln Gly Val Thr Ser Gly Gly
 355 360 365
 Ser Gly Asp Cys Arg Thr Gly Gly Gly Thr Phe Phe Gln Pro Ile Asn
 370 375 380
 Ala Leu Leu Gln Asn Tyr Gly Leu Thr Leu Lys Thr Thr Gly Gly Asp
 385 390 395 400
 Asp Gly Gly Gly Asp Asp Gly Gly Glu Glu Pro Gly Gly Thr Trp Ala
 405 410 415
 Ala Gly Thr Val Tyr Gln Pro Gly Asp Thr Val Thr Tyr Gly Gly Ala
 420 425 430
 Thr Phe Arg Cys Leu Gln Gly His Gln Ala Tyr Ala Gly Trp Glu Pro
 435 440 445
 Pro Asn Val Pro Ala Leu Trp Gln Arg Val
 450 455

<210> 655

<211> 463

<212> PRT

<213> Streptomyces coelicolor A3(2)

<400> 655

Met Pro His Arg His Arg His His Arg Ala Val Gly Ala Ala Val Ala
 1 5 10 15
 Ala Thr Ala Ala Leu Leu Val Ala Gly Leu Ser Gly Ser Ala Ser Ala
 20 25 30
 Gly Thr Ala Pro Ala Gly Ser Ala Pro Thr Ala Ala Glu Thr Leu Arg

<213> Streptomyces griseus

<400> 656

Met	Glu	Arg	Thr	Thr	Leu	Arg	Arg	Arg	Ala	Leu	Val	Ala	Gly	Thr	Ala
1			5					10						15	
Thr	Val	Ala	Val	Gly	Ala	Leu	Ala	Leu	Ala	Gly	Leu	Thr	Gly	Val	Ala
		20					25					30			
Ser	Ala	Asp	Pro	Ala	Ala	Thr	Ala	Ala	Pro	Pro	Val	Ser	Ala	Asp	Ser
		35				40					45				
Leu	Ser	Pro	Gly	Met	Leu	Ala	Ala	Leu	Glu	Arg	Asp	Leu	Gly	Leu	Asp
	50				55				60						
Glu	Asp	Ala	Ala	Arg	Ser	Arg	Ile	Ala	Asn	Glu	Tyr	Arg	Ala	Ala	Ala
65				70					75					80	
Val	Ala	Ala	Gly	Leu	Glu	Lys	Ser	Leu	Gly	Ala	Arg	Tyr	Ala	Gly	Ala
			85					90					95		
Arg	Val	Ser	Gly	Ala	Lys	Ala	Thr	Leu	Thr	Val	Ala	Thr	Thr	Asp	Ala
		100					105					110			
Ser	Glu	Ala	Ala	Arg	Ile	Thr	Glu	Ala	Gly	Ala	Arg	Ala	Glu	Val	Val
		115				120					125				
Gly	His	Ser	Leu	Asp	Arg	Phe	Glu	Gly	Val	Lys	Lys	Ser	Leu	Asp	Lys
	130				135				140						
Ala	Ala	Leu	Asp	Lys	Ala	Pro	Lys	Asn	Val	Pro	Val	Trp	Tyr	Val	Asp
145				150					155					160	
Val	Ala	Ala	Asn	Arg	Val	Val	Val	Asn	Ala	Ala	Ser	Pro	Ala	Ala	Gly
			165					170					175		
Gln	Ala	Phe	Leu	Lys	Val	Ala	Gly	Val	Asp	Arg	Gly	Leu	Val	Thr	Val
		180					185					190			
Ala	Arg	Ser	Ala	Glu	Gln	Pro	Arg	Ala	Leu	Ala	Asp	Ile	Arg	Gly	Gly
	195				200						205				
Asp	Ala	Tyr	Tyr	Met	Asn	Gly	Ser	Gly	Arg	Cys	Ser	Val	Gly	Phe	Ser
	210				215				220						
Val	Thr	Arg	Gly	Thr	Gln	Asn	Gly	Phe	Ala	Thr	Ala	Gly	His	Cys	Gly
225				230					235					240	
Arg	Val	Gly	Thr	Thr	Thr	Asn	Gly	Val	Asn	Gln	Gln	Ala	Gln	Gly	Thr
			245					250					255		
Phe	Gln	Gly	Ser	Thr	Phe	Pro	Gly	Arg	Asp	Ile	Ala	Trp	Val	Ala	Thr
		260					265					270			
Asn	Ala	Asn	Trp	Thr	Pro	Arg	Pro	Leu	Val	Asn	Gly	Tyr	Gly	Arg	Gly
		275				280					285				
Asp	Val	Thr	Val	Ala	Gly	Ser	Thr	Ala	Ser	Val	Val	Gly	Ala	Ser	Val
	290				295					300					
Cys	Arg	Ser	Gly	Ser	Thr	Thr	Gly	Trp	His	Cys	Gly	Thr	Ile	Gln	Gln
305				310					315					320	
Leu	Asn	Thr	Ser	Val	Thr	Tyr	Pro	Glu	Gly	Thr	Ile	Ser	Gly	Val	Thr
			325					330					335		
Arg	Thr	Ser	Val	Cys	Ala	Glu	Pro	Gly	Asp	Ser	Gly	Gly	Ser	Tyr	Ile
		340					345					350			
Ser	Gly	Ser	Gln	Ala	Gln	Gly	Val	Thr	Ser	Gly	Gly	Ser	Gly	Asn	Cys
		355				360					365				
Ser	Ser	Gly	Gly	Thr	Thr	Tyr	Phe	Gln	Pro	Ile	Asn	Pro	Leu	Leu	Gln
	370				375				380						
Ala	Tyr	Gly	Leu	Thr	Leu	Val	Thr	Ser	Gly	Gly	Gly	Thr	Pro	Thr	Asp
385				390					395					400	
Pro	Pro	Thr	Thr	Pro	Pro	Thr	Asp	Ser	Pro	Gly	Gly	Thr	Trp	Ala	Val
			405					410				415			
Gly	Thr	Ala	Tyr	Ala	Ala	Gly	Ala	Thr	Val	Thr	Tyr	Gly	Gly	Ala	Thr

Tyr Arg Cys Leu Gln Ala His Thr Ala Gln Pro Gly Trp Thr Pro Ala
 420 425 430
 435 440 445
 Asp Val Pro Ala Leu Trp Gln Arg Val
 450 455